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10/507416

DT09 Rec'd PCT/PTO 13 SEP 2004

From: CABINET REGIMBEAU

0144293599

10/09/2004 19:30 #035 P.007/095

WO 03/076464

PCT/IB03/01374

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MUTAGENESIS OF *Aspergillus* FUNGI AND GENES ESSENTIAL FOR GROWTH

The present invention is directed to polynucleotides encoding proteins
5 Essential For the Growth (EFG) of filamentous fungi. The invention also deals with
namely polypeptides encoded by said polynucleotides, screening assays for
identifying compounds capable of inhibiting said EFG protein activities,
pharmaceutical or phytosanitary compositions comprising such compounds.

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BACKGROUND

The opportunistic pathogen *Aspergillus fumigatus* is the cause of the most
frequent deadly airborne fungal infection in developed countries. In order to identify
novel antifungal drug targets, the inventors investigated the genome of *A. fumigatus*
for genes that are necessary for efficient fungal growth.

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Aspergillus fumigatus is a saprophytic filamentous fungus that disseminates
through the release of asexual spores (conidia) into air^{1,2}. They are daily inhaled
without major consequences for human health. However, in immuno-compromised
hosts, *A. fumigatus* can cause a usually fatal infection, termed invasive pulmonary
aspergillosis^{1,3} (IPA). With the increasing number of immuno-deficient patients and
20 the development of severe immuno-suppressive therapies, *A. fumigatus* has become
the most prevalent airborne fungal pathogen⁴. Because of a difficult diagnosis during
lifetime and the lack of non-toxic efficient antifungal treatments, IPA is associated
with a mortality rate as high as 85%.

Currently available drugs belong to two families: polyenes (*e.g.*
25 amphotericin B) and azoles (*e.g.* itraconazole), both of them targeting fungal
membranes^{1,5}. Relative toxicity and side effects, in addition to an often-late
diagnostic, limit their use^{1,5}. Recently, new antifungal compounds of the candin
family (caspofungin) which target the enzyme responsible for cell wall $\beta(1,3)$ -glucan
biosynthesis came on the market⁶.

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Besides, *A. fumigatus* is closely related to phytopathogenic fungi. There is a high need of new fungicidal compounds against such fungi. Thus, EFG fungal genes identified by the inventors have a strong utility in the phytopathology field : the identified EFG genes are useful for identifying new fungicidal compositions in screening assays. Knowing the EFG described further, homologous genes of *A. fumigatus* can be isolated from other fungi, namely: *Botrytis cinerea*, *Mycosphaerella graminicola*, *Stagnospora nodorum*, *Blumeria graminis*, *Colleotrichum lindemuthianum*, *Puccinia graminis*, *Leptosphaeria maculans*, *Fusarium oxysporum*, *Fusarium graminearum*, *Venturia inaequalis*, most preferably *Magnaporthe* fungi, even more preferably *Magnaporthe grisea*.

A rational approach to increase the antifungal arsenal relies on the identification of novel targets involved in various aspects of the fungal biology^{7,8}. Although genes necessary for virulence are seen as potential candidates⁹, no genuine virulence factor has been identified in *A. fumigatus* yet^{2,10}. On the other hand, studies which have addressed the role of proposed virulence factors, e.g. adhesins, toxic secondary metabolites or secreted proteases, by direct mutagenesis have only identified genes involved in melanin biosynthesis necessary for conidia pigmentation as important for virulence^{2,37,38,39}. Therefore, it appears that the search for *A. fumigatus* virulence factors has only identified genes that protect conidia from the host response (pigment biosynthesis prevents complement binding and phagocytosis) and metabolic pathway genes (reduced level of an essential nutrient at the site of infection).

Alternative attractive antifungal targets lie among gene products that are essential for fungal growth *ex vivo*^{11,12}. Compendia of essential genes have been obtained for *Saccharomyces cerevisiae* through various approaches including systematic gene inactivation or insertional mutagenesis in a diploid background followed by the analysis of meiotic progenies^{13,14}. More recently, a set of genes critical for growth of the dimorphic yeast *Candida albicans* has also been defined using inducible expression of antisense RNA molecules¹⁵. Among the 86 *C. albicans* genes identified, 38% have no known homologues in available

databases¹⁵. Differences in essential biological processes between the yeasts *S. cerevisiae* and *C. albicans* highlight the need to study the larger and more complex filamentous fungal genomes to reveal species-specific and filamentous-specific targets.

5 *A. fumigatus* is haploid and devoid of a sexual cycle¹⁶, preventing the application of strategies that use classical genetics to define essential genes. The inventors have now demonstrated that the parasexual genetic cycle can be used to demonstrate the essential function of *A. fumigatus* genes. The inventors have used techniques of chemical haploidization of artificial diploid strains^{17,18}. In this
10 setting, a heterozygous *A. fumigatus* diploid is generated by targeted gene replacement or by random insertional mutagenesis and subjected to haploidization with or without the selective pressure corresponding to the introduced mutation. The absence of haploid progenies under selective condition only is indicative of the inactivation of a gene essential for *A. fumigatus* growth (Fig. 1). Using this approach,
15 the inventors have demonstrated that the *FKS1* gene, encoding the 1,3- β -D-glucan synthase catalytic subunit, and the *smcA* gene, encoding a member of the SMC (structural maintenance of chromosome) protein family, are essential for *A. fumigatus* growth. However, their results have shown that the currently used insertional mutagenesis schemes for *A. fumigatus* which rely on integration of a heterologous
20 DNA molecule by DNA-mediated transformation^{19,20} lead to frequent genomic rearrangements that hamper a high-throughput analysis (data not shown). So there was a need for new techniques allowing a reliable identification of EFG genes.

Transposon mutagenesis has been used widely in bacteria^{21,22} and yeasts^{23,24} to elucidate various biological questions but it was only very recently
25 that it has been applied to the filamentous fungus kingdom^{25,26}. In particular, the *impala160* transposable element from *Fusarium oxysporum*, a Class II transposable element of the *Tc1-mariner* family²⁷, has been shown to transpose efficiently in *Fusarium* species²⁸, *A. nidulans*²⁹ and *Magnaporthe grisea*³⁰. However, transposon mutagenesis has not been used yet for a reliable identification of genes essential for
30 growth of *Aspergillus* fungi, especially *A. fumigatus*. Such identification needs appropriated protocol settings and is absolutely not obvious, practically speaking.

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Furthermore, as it will be shown, the EFG genes of *A. fumigatus* identified by the inventors were until now not known, and some of them are surprisingly totally specific for Aspergilli or for filamentous ascomycetes, being not found in ascomycetous yeasts. The new EFG genes from *A. fumigatus* described in this application are as such neither described nor suggested in the prior art.

SUMMARY OF THE INVENTION

The inventors have succeeded in the identification of EFG genes, by using an *in vivo* transposon mutagenesis system for *A. fumigatus*. The inventors have shown that *impala160* (see FR 2 791 361) and its derivatives also transpose in *A. fumigatus* and can be used to generate a collection of random heterozygous diploids. Screening by parasexual genetics of such a collection has resulted in the complete characterization without prior sequence information of 210 new *A. fumigatus* genes which are necessary for efficient fungal growth.

The present invention thus pertains, according to a first aspect, to nucleic acid molecules, including in particular the complete cDNA sequence, encoding the EFG protein, as well as the corresponding translation product. Oligonucleotide probes or primers hybridizing specifically with a EFG genomic DNA or cDNA sequence are also part of the present invention, as well as DNA amplification and detection methods using said primers and probes.

A further aspect of the invention consists of recombinant vectors comprising any of the nucleic acid sequences described above, and in particular of recombinant vectors comprising a EFG regulatory sequence or a sequence encoding a EFG protein, as well as of cell hosts comprising said nucleic acid sequences or recombinant vectors.

The invention is also directed to methods for the screening of substances or molecules that inhibit the expression of the EFG genes, as well as with methods for the screening of substances or molecules that interact with and/or inhibit the activity of a EFG polypeptide.

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Another object of the invention is to develop new compositions, either pharmaceutical or phytosanitarical, capable of inhibiting or preferably completely suppressing the toxic effect of filamentous fungi.

More precisely, the invention relates, according to a first aspect, to a nucleic acid encoding an Essential For Growth (EFG) polypeptide selected from the group consisting of :

(i) a nucleic acid molecule encoding a polypeptide comprising the amino acid sequence depicted in one of SEQ ID N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114, 118,122,126,130,134,138,142,146,150,154,158,162,166,170 ;

(ii) a nucleic acid molecule comprising the nucleic acid sequence as depicted in one of SEQ ID N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112, 116,120,124,128,132,136,140,144,148,152,156,160,164,168 ;

(iii) a nucleic sequence having at least 80, 85, 90, 95, 98, 99% identity with a sequence of SEQ ID N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112, 116,120,124,128,132,136,140,144,148,152,156,160,164,168 ;

(iv) a nucleic acid molecule which hybridizes under stringent conditions to

(a) a nucleic acid as defined in (i), (ii) and (iii), or

(b) a complementary strand of (a) ;

(v) a nucleic acid the sequence of which is degenerated as a result of the genetic code to the sequence of a nucleic acid as defined in (i), (ii), (iii) and (iv).

The invention also relates to an isolated nucleic acid, said nucleic acid comprising a nucleotide sequence encoding:

i) a EFG polypeptide comprising an amino acid sequence having at least 80% identity to a sequence of SEQ ID N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118,122,126,130,134,138,142,146,150,154,158,162,166,170 ; or

ii) a biologically active fragment of said polypeptide.

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The invention also relates to an isolated nucleic acid, said nucleic acid comprising a nucleotide sequence encoding:

- i) a EFG polypeptide comprising an amino acid sequence which is orthologous to a sequence of SEQ ID N°3, 6, 9, 12, 15, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45, 48, 51, 54, 57, 60, 94, 98, 102, 106, 110, 114, 118, 122, 126, 130, 134, 138, 142, 146, 150, 154, 158, 162, 166, 170; or
- ii) a biologically active fragment of said polypeptide.

The invention also relates to an isolated nucleic acid sequence mentioned above encoding a polypeptide of *A. fumigatus* exhibiting a biological function associated to fungal growth, said nucleic acid comprising a sequence of SEQ ID N°2, 5, 8, 14, 17, 20, 23, 26, 29, 32, 35, 38, 41, 44, 47, 50, 53, 56, 59, 93, 97, 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, 141, 145, 149, 153, 157, 161, 165, 169. The sequences of SEQ ID N°2, 5, 8, 14, 17, 20, 23, 26, 29, 32, 35, 38, 41, 44, 47, 50, 53, 56, 59, 93, 97, 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, 141, 145, 149, 153, 157, 161, 165, 169 are issued respectively from the sequences of SEQ ID N°1, 4, 7, 10, 13, 16, 19, 22, 25, 28, 31, 34, 37, 40, 43, 46, 49, 52, 55, 58, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 132, 136, 140, 144, 148, 152, 156, 160, 164, 168, and are also defined as ORF

ORF (open reading frame) are representative fragments of the EFG genes of the invention, between a start codon and a stop codon or between two stop codons encoding the EFG polypeptides of the invention.

The biological function associated to fungal growth is preferably chosen in the group consisting of protein synthesis, protein maturation, protein transport, nuclear architecture, RNA processing, nucleotide metabolism, chromatine structure, cell cycle control.

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The invention also relates to said nucleic acid operably linked to a promoter, to an expression cassette comprising said nucleic acid, to a host cell comprising said expression cassette.

According to another aspect the invention relates to a biologically active
5 polypeptide encoded by a nucleic acid described above.

The invention also relates to a polypeptide comprising an amino acid sequence of at least 80% amino acid sequence identity to a sequence of SEQ ID N°3, 6, 9, 12, 15, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45, 48, 51, 54, 57, 60, 94, 98, 102, 106, 110, 114, 118, 122, 126, 130, 134, 138, 142, 146, 150, 154, 158, 162, 166, 170.

10 According to a further aspect, the invention relates to a method of identifying a candidate inhibitor of EFG polypeptide, said method comprising:

- i) contacting a EFG polypeptide according to claim 5 or 6 with a test compound ;
- ii) determining whether said compound selectively binds to said polypeptide, said binding indicating that said compound is a candidate inhibitor.

15 The invention also relates to a method of identifying a candidate inhibitor of EFG polypeptide, said method comprising:

- a) contacting said polypeptide with a test compound;
- b) determining whether said compound selectively inhibits the activity of said polypeptide, said inhibition indicating that said compound is a candidate inhibitor.

20 According to a further aspect, the invention relates to a method for locating at least one gene essential for the growth of a haploid fungus, said method comprising the following successive steps:

- generation of diploid strain from haploid fungal strain ;
 - mutagenesis of said diploid strain;
 - 25 - haploidisation of the diploid transformant strain, in selection conditions such that the absence of haploid progeny is indicative of mutagenesis occurring in said essential gene;
- said mutagenesis being an *in vivo* transposon mutagenesis.

30 Preferably, the fungus belongs to the *Aspergillus* genus or the *Penicillium* genus. Preferably, the fungus is *Aspergillus fumigatus*.

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Preferably, the transposon is the *impala160* transposon or its derivatives, the selection medium is a benomyl-containing medium, the transposon *impala160* is carried by a plasmid pNlpyr, the diploid strain is chosen between CEA225, CEA 226, CEA 227, and CEA 280:

- 5 -strain DH5a (pNlpyr): this strain (CNCM I-2815) is derivated from strain DH5a of *E. coli* K-12 transformed by a derivative of pBR322 carrying the *impala160* transposon of *Fusarium oxysporum*, in which has been inserted the *pyrG* gene of *Aspergillus nidulans*; transformed in a *niaD*- *pyrG*- of *Aspergillus fumigatus*, this plasmid confers prototrophy to uridin and uracil, and allows to select transposition of
- 10 *impala160::pyr* by growth in a medium that contains nitrate as the sole nitrogen source.
- CEA 225 (CNCM I-2816), CEA 226 (CNCM I-2817), CEA 227 (CNCM I-2818), and CEA 280 are diploid strains of *Aspergillus fumigatus* derivated from the strain CBS144-89 by gene transformation, spontaneous mutagenesis, cross and
- 15 transformation by plasmid pNlpyr. Genotype: *pyrG1/pyrG1 w1/F2/+ +/r7F1 cnx1/+ niaD1/niaD2 X/X::pNlpyr*.

The invention also provides a method for locating at least one gene essential for the growth of a fungus of the *Penicillium* genus which exhibits a parasexual cycle and the diploids of which are stable.

- 20 Further, the heterozygous diploid strains are useful tools for direct screening of active molecules against *A. fumigatus*. Accordingly, the invention provides a method of screening of compounds that are active against *A. fumigatus* comprising:
- preparing an *A. fumigatus* strain that is heterozygous for an EFG gene (heterozygous EFGn/efgn);
 - 25 - preparing an *A. fumigatus* strain that is homozygous for the EFG gene (homozygous EFGn/EFGn);
 - comparing the effect of a candidate compound on the heterozygous EFGn/efgn and on the homozygous EFGn/EFGn,
- the higher inhibiting effect on the heterozygous EFGn/efgn than on the homozygous
- 30 EFGn/EFGn indicating that the compound is an inhibitor.

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This method involves typically the comparison for one EFG gene (for instance for EFG1 gene (n=1), comparison between EFG1/efg1 strain and EFG1/EFG1 strain).

Thus, a population of heterozygous diploid *A. fumigatus* G/g::impala can be screened
5 in order to identify one or more strains that are more sensitive to a fungicidal compound which action mechanism is unknown : the characterization of the gene G will allow to identify the action mechanism of said fungicidal compound.

According to a further aspect, the invention relates to an isolated nucleic acid sequence described above, obtainable by a method of locating described above.

10 According to a further aspect, the invention relates to a composition capable of inhibiting haploid fungal growth, said composition comprising at least one compound capable of inhibiting the expression of at least one EFG gene the nucleic acid sequence of which is described above.

The composition is typically either pharmaceutical or fungicidal.

15

BRIEF DESCRIPTION OF THE SEQUENCE LISTING

SEQ

ID

N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,
116,120,124,128,132,136,140,144,148,152,156,160,164,168 are cDNA sequences
20 encoding *Aspergillus fumigatus* EFG protein. In the whole application, the expression

“SEQ

ID

N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,
116,120,124,128,132,136,140,144,148,152,156,160,164,168” means the group
consisting of SEQ ID N°1, SEQ ID N°4, SEQ ID N°7, SEQ ID N°10, SEQ ID
25 N°13, SEQ ID N°16, SEQ ID N°19, SEQ ID N°22, SEQ ID N°25, SEQ ID N°28,
SEQ ID N°31, SEQ ID N°34, SEQ ID N°37, SEQ ID N°40, SEQ ID N°43, SEQ ID
N°46, SEQ ID N°49, SEQ ID N°52, of SEQ ID N°55, SEQ ID N°58, SEQ ID N°92,
SEQ ID N°96, SEQ ID N°100, SEQ ID N°104, SEQ ID N°108, SEQ ID N°112,
SEQ ID N°116, SEQ ID N°120, SEQ ID N°124, SEQ ID N°128, SEQ ID N°132,
30 SEQ ID N°136, SEQ ID N°140, SEQ ID N°144, SEQ ID N°148, SEQ ID N°152,
SEQ ID N°156, SEQ ID N°160, of SEQ ID N°164, SEQ ID N°168.

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SEQ ID
 N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,
 118,122,126,130,134,138,142,146,150,154,158,162,166,170 are the amino acid
 sequences of *Aspergillus fumigatus* EFG polypeptides. In the whole application, the
 5 expression "SEQ ID
 N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,
 118,122,126,130,134,138,142,146,150,154,158,162,166,170" means the group
 consisting of SEQ ID N°3, SEQ ID N°6, SEQ ID N°9, SEQ ID N°12, SEQ ID
 N°15, SEQ ID N°18, SEQ ID N°21, SEQ ID N°24, SEQ ID N°27, SEQ ID N°30,
 10 SEQ ID N°33, SEQ ID N°36, SEQ ID N°39, SEQ ID N°42, SEQ ID N°45, SEQ ID
 N°48, SEQ ID N°51, SEQ ID N°54, of SEQ ID N°57, SEQ ID N°60, SEQ ID N°94,
 SEQ ID N°98, SEQ ID N°102, SEQ ID N°106, SEQ ID N°110, SEQ ID N°114,
 SEQ ID N°118, SEQ ID N°122, SEQ ID N°126, SEQ ID N°130, SEQ ID N°134,
 SEQ ID N°138, SEQ ID N°142, SEQ ID N°146, SEQ ID N°150, SEQ ID N°154,
 15 SEQ ID N°158, SEQ ID N°162, of SEQ ID N°166, SEQ ID N°170.

An analogous construction is to be applied when having the expression "SEQ
 ID
 N°2,5,8,14,17,20,23,26,29,32,35,38,41,44,47,50,53,56,59,93,97,101,105,109,113,11
 7,121,125,129,133,137,141,145,149,153,157,161,165,169".

20

Table 1. *A. fumigatus* essential genes^a

^aFor each identified integration of *impala160::pyrG*, the corresponding TIGR contig
 number is indicated (www.tigr.org) with its length (kb) and the position of the TA
 where transposon integration occur (bp).

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Table 1

		<i>A. fumigatus</i> genome sequence version of November 2001							<i>A. fumigatus</i> genome sequence version of February 2003						
Clone Id	Strain Id	Nucl etc acid SEQ ID	ORF SEQ ID	Amin o acid SEQ ID	Contig TIGR n°	Contig length (kb)	impalal60::p yrG location	gene SEQ_ ID	Nucl etc acid SEQ ID	ORF SEQ ID	Amin o acid SEQ ID	Contig TIGR n°	Contig length (kb)	Coordinates of gene SEQ_ID on contig	impalal60::p yrG location
10-80	CEA231	1	2	3	131	27.2	15399	103	104	105	106	4940	205712	54154-50350	53934
10-291	CEA233	4	5	6	164	45.3	40601	111	112	113	114	4865	598154	3495-6359	4705
7-1-19	CEA254	7	8	9	43	93.1	72592	119	120	121	122	4911	85632	43163-41221	42151
10-3-7	CEA255	10	11	12	408	71.1	53190	123	124	125	126	4899	1041326	441274- 438167	440657
2-6-4	CEA256	13	14	15	110	207.8	105657	127	128	129	130	4938	1796676	582107- 579544	581561
2-1-1	CEA257	16	17	18	493	42.2	14886	131	132	133	134	4951	825238	8362-11737	11010
2-10- 16	CEA258	19	20	21	190	22.1	7131	135	136	137	138	4912	206341	46084-42446	43492
5-4-21	CEA259	22	23	24	1327	4.7	2928	139	140	141	142	4963	622595	373462- 376145	375531
2-10- 21	CEA260	25	26	27	493	42.8	36145	143	144	145	146	4849	22910	12560-15101	13405
7-5-9	CEA261	28	29	30	93	53.7	11506	147	148	149	150	4857	591293	164191- 165827	164994
10-2- 18	CEA262	31	32	33	1366	3.6	1870	151	152	153	154	4903	416417	3571-1535	3157
9-11	CEA230	34	35	36	1754	6.3	603	99	100	101	102	4899	1041326	9642-7242	7285
4-3-3	CEA263	37	38	39	838	9.8	8261	155	156	157	158	4944	310661	159432- 161250	159931
11-6- 11	CEA264	40	41	42	846	16.7	3278	159	160	161	162	4899	1041326	65039-62439	64261
8-47	CEA228	43	44	45	960	5.1	223	91	92	93	94	4842	368858	234347- 231296	234245

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Table 1 (continued)

10-304	CEA234	46	47	48	408	71.1	55903	115	116	117	118	4899	1041326	443110- 444619	443430
10-175	CEA232	49	50	51	221	76.1	67069	107	108	109	110	4938	1796676	211008- 213420	211352
11-4-9	CEA265	52	53	54	573	36.5	13244	163	164	165	166	4826	811005	355652- 358190	356111
2-10- 18	CEA266	55	56	57	585	39.5	24940	167	168	169	170	4898	422562	329309- 331987	330474
8-62	CEA229	58	59	60	221	76.1	60969	95	96	97	98	4938	1796676	215653- 219466	217453
6-8-13	CEA280				6	212.7	208370	171	172	173	174	4925	1083193	997952- 996381	997591
5-3-11	CEA281. 1				792	13.7	1353	175	176	177	178	4839	130518	10030-12622	12332
5-3-11	CEA281. 2				792	13.7	1353	179	180	181	182	4839	130518	12269-14135	12332
10-4- 20	CEA282. 1				443	89.1	67662	183	184	185	186	4929	586561	328110- 325663	328147
10-4- 20	CEA282. 2				443	89.1	67662	187	188	189	190	4929	586561	328075- 330267	328147
11-6- 20	CEA283				716	14.3	9480	191				4910	185565	9638-11637	10637
4-3-4	CEA284. 1				652	29.4	18411	192	193	194	195	4899	1041326	472441- 476776	476988
4-3-4	CEA284. 2				652	29.4	18411	196	197	198	199	4899	1041326	477626- 479684	476988

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Table 1 bis

Clone Id	Protein Id	March 2002 Amino acid SEQ ID	March 2003 Amino acid SEQ ID	Size introns +exons (nt)	Size protein (aa)	Location of imp160::pyr A in start codon (nt)	S. cerevisiae closest homologue	Essential in S. cerevisiae	Function	Functional category
10-80	CEA231_prot	3	106	2805	934	-280	DBP10/YDL031w	yes	ATP-dependent RNA helicase	RNA processing
10-291	CEA233_prot	6	114	1865	574	733	NAR1/YNL240c	yes	Nuclear architecture related protein	Nuclear architecture
7-1-19	CEA254_prot	9	122	943	200	511	GUK1/YDR454c	yes	Guanylate kinase	Nucleotide metabolism
10-3-7	CEA255_prot	12	126	2108	657	57	SRP101/YDR292c	yes	Signal recognition particle receptor - alpha subunit	Protein transport
2-6-4	CEA256_prot	15	130	1564	460	46	WBP1/YEL002c	yes	Oligosaccharyl transferase beta subunit	Protein modification
2-1-1	CEA257_prot	18	134	2376	715	2148	YGL245w	yes	Glutamate-tRNA synthetase	Protein synthesis
2-10-16	CEA258_prot	21	138	2639	809	2191	CDC27/YBL084c	yes	Cell division control protein	Cell cycle control
5-4-21	CEA259_prot	24	142	1707	568	1569	RSC9/YML127w	yes	Component of the chromatin remodeling complex	Chromatin structure
2-10-21	CEA260_prot	27	146	1542	493	345	SPE2/YOL052c	yes	S-adenosylmethionine decarboxylase	Metabolism
7-5-9	CEA261_prot	30	150	637	139	303	RPL17A/YKL180w	no	Ribosomal protein of the large subunit of the ribosome (L17)	Protein synthesis
10-2-18	CEA262_prot	33	154	1037	256	-131	RPL17B/YJL177w	no	Ribosomal protein of the large subunit of the ribosome (L17)	Protein synthesis
9-11	CEA230_prot	36	102	1401	399	1316	RPL1A/YGL135w	no	Ribosomal protein of the large subunit of the ribosome (L1)	Protein synthesis
4-3-3	CEA263_prot	39	158	819	227	-1	MSW1/YDR268w	no	Mitochondrial tryptophanyl-tRNA synthetase	Protein synthesis
11-6-11	CEA264_prot	42	162	1601	394	278	GOS1/YHL031c	no	SNARE protein	Protein transport
8-47	CEA228_prot	45	94	2052	683	-398	RIM11/YMR139w	no	Serine/threonine-protein kinase	Cell cycle control
							YFL034w	no	Probable membrane protein. Yfl034wp	Unknown

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Table 1 bis (continued)

10-304	CEA234 _prot	48	118	461	141	-179	RPL14A/YHL001 w	no	Ribosomal protein of the large subunit of the ribosome (L14)	Protein synthesis
10-175	CEA232 _prot	51	110	1413	428	-105	RPL14B/YKL006w	yes	Ferrochelatase	Heme biosynthesis
11-4-9	CEA265 _prot	54	166	1539	512	-40	HEM15/YOR176w	no	Prothymine IX farnesyltransferase	Heme biosynthesis
2-10-18	CEA266 _prot	57	170	1629	542	195	COX10/YPL172c	no	Topoisomerase	DNA replication
8-62	CEA229 _prot	60	98	2814	937	1300	TRF4/YOL115w	no	unknown function	Unknown
6-8-13	CEA280 _prot		174	573	190	138	no hit found	no	weak homology to S. pombe GTPase activator protein and to myocilin	unknown
5-3-11	CEA281. 1_prot		178	1974	609	2037	PAC2/YER007w	no	tubulin folding cofactor E	Cytoskeleton
5-3-11	CEA281. 2_prot		182	963	291	-290	no hit found		unknown function	unknown
10-4-20	CEA282. 1_prot		186	1448	464	-537	PBP2/YBR233w	no	hnRNP complex protein/PAB1-binding protein	RNA processing
10-4-20	CEA282. 2_prot		190	1143	344	-427	SEC3/YER008c	yes	unknown function	Protein secretion
4-3-4	CEA284. 1_prot		195	3336	1059	4049	ENAS/YDR038c	no	P-type ATPase	Ion transport
4-3-4	CEA284. 2_prot		199	1059	352	-1137	no hit found		secondary metabolite biosynthesis protein	unknown

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BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1: Strategy for the identification of essential genes in *A. fumigatus*.

A stable diploid strain heterozygous for spore color markers (*wl*, *r7*) is randomly
5 mutagenized with the transposable element *impala160::pyrG* (*imp::pyr*). During
haploidization on benomyl containing media, random loss of chromosomes gives rise to
two sub-populations of colored haploid conidia (*wl* or *r7*): one bearing the transposon-
inactivated allele (population A) and one bearing wild type allele (population B). The
ability to form haploid progenies on non selective haploidization medium and the
10 inability on selective haploidization medium (without uridine and uracile) leads to the
identification of mutant strains with an insertion in an essential gene.

Figure 2: *In vivo* random transposon mutagenesis in *A. fumigatus*.

(A) Schematic representation of *impala160::pyrG* transposition in a *A. fumigatus* strain
transformed by pNIpyr. Expression of the nitrate reductase gene (*niaD*) is prevented by
15 the presence of the transposable element *impala160::pyrG* (*imp::pyr*) into the promoter
region. Positive selection of transposition events is obtained by selection of nitrate-
utilizing revertants which appear as a result of the excision of *imp::pyr* and the restoration
of a functional *niaD* promoter. Selection of *imp::pyr* reintegration events is ensured by
the presence of *pyrG* in the transposable element when transposition events are induced in
20 a *A. fumigatus pyrG* strain and in the absence of uridine and uracile. (B) Southern blot
analysis of parental diploid transformants (lane 1: CEA225; lane 4: CEA226; lane 7:
CEA227) and diploid revertants (lane 2: Rev 225-1; lane 3: Rev 225-2; lane 5: Rev 226-
1; lane 6: Rev 226-2; lane 8: Rev 227-1; lane 9: Rev 227-2). Hybridization with a probe
for *impala160::pyrG* revealed integration of the transposable element into the promoter
25 of the *niaD* gene in the three parental transformants (arrowheads) and integration at
apparent random sites in the genome of the diploid revertants.

Figure 3: Parasexual screening. Haploidization of 10 diploid revertants on non-
selective (A) and selective (B) media.

Random segregation of chromosomes is visualized by the production of differently
30 colored haploid conidia (see Fig.1: allele *wl* and *r7*). On selective haploidization
medium, in the case of plasmid integration in an essential gene, a residual growth

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phenotype is observed (arrowheads). For these revertants, haploid spores obtained on non selective haploidization medium were tested for the absence of the transposable element in order to confirm the essential phenotype.

5 DETAILED DESCRIPTION OF THE INVENTION

The present invention is based on the discovery of novel molecules, referred to herein as EFG protein and nucleic acid molecules, encoding proteins Essential For Growth expressed in *Aspergillus fumigatus*.

10 An artificial *A. fumigatus* diploid strain with one copy of the *impala160* transposon from *Fusarium oxysporum* integrated into its genome was used to generate a library of diploid strains with random transposon integration. Among *ca.* 2,300 heterozygous diploid strains screened by parasexual genetics, 1.2% have a copy of the transposable element integrated into a gene essential for fungal growth. Homologues of genes essential for *Saccharomyces cerevisiae* growth have been identified, as well as
15 genes that do not share homologues in other fungal species.

The term "EFG genes" refers to genes that are necessary for efficient fungal growth. An efficient growth refers to the normal growth of this fungus in absence of inhibitor of at least one of these genes. Inhibitors may be used to inhibit normal expression of at least one of the EFG genes identified herein.

20 Isolated EFG proteins of the present invention, have an amino acid sequences sufficiently homologous to the amino acid sequence of SEQ ID N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118, 122,126,130,134,138,142,146,150,154,158,162,166,170, or are encoded by a nucleotide sequence sufficiently homologous to one of SEQ ID
25 N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116, 120,124,128,132,136,140,144,148,152,156,160,164,168. As used herein, the term "sufficiently homologous" refers to a first amino acid or nucleotide sequence which contains a sufficient or minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain) amino acid residues or nucleotides to a second
30 amino acid or nucleotide sequence such that the first and second amino acid or nucleotide sequences share common structural domains or motifs and/or a common functional

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activity. For example, amino acid or nucleotide sequences which share common structural domains have at least about 30-40% identity, preferably 40-50% identity, more preferably 50-60%, and even more preferably 60-70%, 70-80%, 80, 90%, 95%, 97%, 98%, 99% or 99.8% identity across the amino acid sequences of the domains are defined herein as sufficiently homologous. Furthermore, amino acid or nucleotide sequences which share at least 30%, preferably 40%, more preferably 60%, 70%, 80%, 90%, 95%, 97%, 98%, 99% or 99.8% identity and share a common functional activity are defined herein as sufficiently homologous.

Homologues are thus defined as those genes or gene products that show a significant level of identity or similarity at the nucleotide or amino acid level, respectively, as indicated above.

Orthologous genes are defined herein as those genes or gene products from two different species which, upon individual comparison to the gene set of the other species, appear reciprocally as the closest homologues.

As used interchangeably herein, a "EFG activity", "biological activity of EFG" or "functional activity of EFG", refers to an activity exerted by a EFG protein, polypeptide or nucleic acid molecule as determined *in vivo*, or *in vitro*, according to appropriate techniques.

The level of inhibition of EFG activity may depend on the number of the EFG genes that are inhibited and on the EFG genes inhibited. The inhibition of at least one EFG gene results in an inhibition of at least 5, 10, 20, 40, 60, 80, 90, 95% of the efficient growth. Preferably, the inhibition is of 100%, meaning the total suppression of growth and of the toxic effect of the fungus.

In one embodiment, a EFG activity is a direct activity, such as an association with a EFG-target molecule or most preferably EFG activity. As used herein, a "target molecule" is a molecule with which a EFG protein binds or interacts in nature, such that EFG-mediated function is achieved. Alternatively, a EFG activity is an indirect activity, such as an activity mediated by interaction of the EFG protein with a EFG target molecule such that the target molecule modulates a downstream cellular activity (*e.g.*, interaction of an EFG molecule with a EFG target molecule can modulate the activity of that target molecule on an intracellular signaling pathway).

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I. EFG Nucleic Acids

The inventors have identified and completely characterized 21 EFG cDNA indicated in Table 1 and Table 1bis. For instance EFG2 refers to a 1735 nucleotide (nt) sequence in length (SEQ ID N°4) which comprises the nucleic acid of SEQ ID N°5 of 1592 nt in length, which encodes the protein of SEQ ID N°6, which is 530 amino acid residues in length.

One aspect of the invention pertains to purified or isolated nucleic acid molecules that encode EFG proteins or biologically active portions thereof, as well as nucleic acid fragments thereof. Fragments may be used for example as hybridization probes to identify EFG-encoding nucleic acids (e.g., EFG mRNA) and fragments for use as probes (e.g. for detection of EFG nucleic acid molecules) or primers (e.g. for sequencing, genotyping, amplification or mutation of EFG nucleic acid molecules). As used herein, the term "nucleic acids" and "nucleic acid molecule" is intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. Throughout the present specification, the expression "nucleotide sequence" may be employed to designate indifferently a polynucleotide or a nucleic acid. More precisely, the expression "nucleotide sequence" encompasses the nucleic material itself and is thus not restricted to the sequence information (i.e., the succession of letters chosen among the four base letters) that biochemically characterizes a specific DNA or RNA molecule. Also, used interchangeably herein are terms "nucleic acids", "oligonucleotides", and "polynucleotides".

An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of

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chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, e.g., a nucleic acid molecule having a nucleotide sequence of SEQ ID N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116,
5 120,124,128,132,136,140,144,148,152,156,160,164,168, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or portion of the nucleic acid sequence of SEQ ID N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116,
10 120,124,128,132,136,140,144,148,152,156,160,164,168, as a hybridization probe, EFG nucleic acid molecules can be isolated using standard hybridization and cloning techniques (e.g., as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. Molecular Cloning. A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989).

Moreover, a nucleic acid molecule encompassing all or a portion of a sequence of
15 SEQ ID N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116, 120,124,128,132,136,140,144,148,152,156,160,164,168, can be isolated by the polymerase chain reaction (PCR) using synthetic oligonucleotide primers designed based upon a sequence of SEQ ID
20 N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116, 120,124,128,132,136,140,144,148,152,156,160,164,168.

A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be
25 cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to EFG nucleotide sequences can be prepared by standard synthetic techniques, e.g., using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises, consists essentially of, or consists of the nucleotide sequence of SEQ ID
30 N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116, 120,124,128,132,136,140,144,148,152,156,160,164,168, or fragments thereof. The

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sequences of SEQ ID
N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116,
120,124,128,132,136,140,144,148,152,156,160,164,168, correspond to *A. fumigatus* EFG
cDNA.

5 Also encompassed by the EFG nucleic acids of the invention are nucleic acid
molecules which are complementary to EFG nucleic acids described herein. Preferably, a
complementary nucleic acid is sufficiently complementary to a nucleotide sequence of
SEQ ID
N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116,
10 120,124,128,132,136,140,144,148,152,156,160,164,168, such that it can hybridize to a
nucleotide sequence of SEQ
N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116,
120,124,128,132,136,140,144,148,152,156,160,164,168.

Another object of the invention is a purified, isolated, or recombinant nucleic acid
15 encoding a EFG polypeptide comprising an amino acid sequence of SEQ ID
N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118,
122,126,130,134,138,142,146,150,154,158,162,166,170, or fragments thereof. Preferred
polynucleotides of the invention also include purified, isolated, or recombinant EFG
cDNAs consisting of, consisting essentially of, or comprising a sequence of SEQ ID
20 N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116,
120,124,128,132,136,140,144,148,152,156,160,164,168. Particularly preferred nucleic
acids of the invention include isolated, purified, or recombinant polynucleotides
comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90,
100, 150, 200, 500, 1000 or 2000 nucleotides (upper lengths of the fragments to be
25 adapted to the length of the nucleotide sequence) of a sequence of SEQ ID
N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116,
120,124,128,132,136,140,144,148,152,156,160,164,168, or the complements thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion
of a nucleic acid sequence of SEQ ID
30 N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116,
120,124,128,132,136,140,144,148,152,156,160,164,168, for example a fragment which

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can be used as a probe or primer or a fragment encoding a biologically active portion of a EFG protein. The nucleotide sequence determined from the cloning of the EFG genes allows for the generation of probes and primers designed for use in identifying and/or cloning other EFG family members, as well as EFG homologues from other species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sequence of SEQ ID N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116, 120,124,128,132,136,140,144,148,152,156,160,164,168, or a sequence complementary thereto.

A nucleic acid fragment encoding a "biologically active portion of a EFG protein" can be prepared by isolating a portion of a nucleotide sequence of SEQ ID N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116, 120,124,128,132,136,140,144,148,152,156,160,164,168, which encodes a polypeptide having a EFG biological activity (the biological activities of the EFG proteins described herein), expressing the encoded portion of the EFG protein (e.g., by recombinant expression in vitro) and assessing the activity of the encoded portion of the EFG protein.

The invention further encompasses nucleic acid molecules that differ from a nucleotide sequence of SEQ ID N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116, 120,124,128,132,136,140,144,148,152,156,160,164,168, due to degeneracy of the genetic code and thus encode the same EFG proteins as those encoded by a nucleotide sequence of SEQ ID N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116, 120,124,128,132,136,140,144,148,152,156,160,164,168. In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence encoding a protein having an amino acid sequence of SEQ ID N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118, 122,126,130,134,138,142,146,150,154,158,162,166,170.

In addition to the EFG nucleotide sequences of SEQ ID

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N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116, 120,124,128,132,136,140,144,148,152,156,160,164,168, it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of the EFG proteins may exist within a population (e.g., the fungal population). Such genetic polymorphism in the EFG genes may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an EFG protein, preferably a fungal EFG protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of a EFG gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in EFG genes that are the result of natural allelic variation and, most preferably, that do not alter the functional activity of a EFG protein are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural allelic variants and homologues of the EFG cDNAs of the invention can be isolated based on their homology to the EFG nucleic acids disclosed herein using the cDNAs disclosed herein, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 70%, more preferably at least about 80%, even more preferably at least about 85%, 90%, 95% or 98% homologous to each other typically remain hybridized to each other. Stringent conditions are known to those skilled in the art and can be found in Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6 * sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 *SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of SEQ ID NO:1 corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to a RNA or DNA molecule having a nucleotide sequence that occurs in nature

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(e.g., encodes a natural protein).

In addition to naturally-occurring allelic variants of the EFG sequences that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into a nucleotide sequence of SEQ ID
5 N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116,
120,124,128,132,136,140,144,148,152,156,160,164,168, thereby leading to changes in
the amino acid sequence of the encoded EFG proteins, without altering the functional
ability of the EFG proteins. For example, nucleotide substitutions leading to amino acid
substitutions at "non-essential" amino acid residues can be made in a sequence of
10 N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118,
122,126,130,134,138,142,146,150,154,158,162,166,170. A "non-essential" amino acid
residue is a residue that can be altered from the wild-type sequence of EFG (e.g., the
sequence of SEQ ID NO:1) without altering the biological activity, whereas an "essential"
amino acid residue is required for biological activity. For example, amino acid residues
15 that are conserved among the EFG proteins of the present invention, are predicted to be
less unamenable to alteration. Furthermore, additional conserved amino acid residues may
be amino acids that are conserved between the EFG proteins of the present invention and
other members of the *Aspergillus* family and/or of other fungi.

Thus, the invention further encompasses nucleic acid molecules that are
20 homologous to the nucleic acids of *A. fumigatus* described above and that are isolated
from target phytopathogenic fungi, namely *Botrytis cinerea*, *Mycosphaerella*
graminicola, *Stagnospora nodorum*, *Blumeria graminis*, *Colleotrichum lindemuthianum*,
Puccinia graminis, *Leptosphaeria maculans*, *Fusarium oxysporum*, *Fusarium*
graminearum, *Venturia inaequalis*, most preferably fungi of the genus *Magnaporthe*,
25 even most preferably *Magnaporthe grisea*.

Accordingly, another aspect of the invention pertains to nucleic acid molecules
encoding EFG proteins and biologically active fragments thereof that contain changes in
amino acid residues that are not essential for activity. Such EFG proteins differ in amino
acid sequence of SEQ ID
30 N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118,
122,126,130,134,138,142,146,150,154,158,162,166,170, yet retain biological activity. In

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one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 60% homologous to an amino acid sequence of SEQ ID N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118, 122,126,130,134,138,142,146,150,154,158,162,166,170. Preferably, the protein encoded by the nucleic acid molecule is at least about 65-70% homologous to a sequence of SEQ ID N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118, 122,126,130,134,138,142,146,150,154,158,162,166,170, more preferably sharing at least about 75-80% identity with SEQ ID N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118, 122,126,130,134,138,142,146,150,154,158,162,166,170, even more preferably sharing at least about 85%, 90%, 92%, 95%, 97%, 98%, 99% or 99.8% identity with a sequence of SEQ ID N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118, 122,126,130,134,138,142,146,150,154,158,162,166,170.

An isolated nucleic acid molecule encoding a EFG protein homologous to a protein of SEQ ID N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118, 122,126,130,134,138,142,146,150,154,158,162,166,170, can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of SEQ ID N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116, 120,124,128,132,136,140,144,148,152,156,160,164,168, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into a sequence of N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116, 120,124,128,132,136,140,144,148,152,156,160,164,168, by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue

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is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in a EFG protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a EFG coding sequence, such as by saturation mutagenesis. Following mutagenesis the encoded protein can be expressed recombinantly and the activity of the protein can be determined.

The biological EFG activity of the protein fragments and mutants described above can be assayed according to the tests known from the one skilled in the art.

Primers and probes of the invention can be prepared by any suitable method, including, for example, cloning and restriction of appropriate sequences and direct chemical synthesis by a method such as the phosphodiester method of Narang SA, Hsiung HM, Brousseau R, Methods Enzymol 1979;68:90-98, the phosphodiester method of Brown EL, Belagaje R, Ryan MJ, Khorana HG, Methods Enzymol 1979;68:109-151, the diethylphosphoramidite method of Beaucage et al., Tetrahedron Lett 1981, 22: 1859-1862 and the solid support method described in EP 0 707 592.

Any of the polynucleotides of the present invention can be labeled, if desired, by incorporating any label known in the art to be detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For example, useful labels include radioactive substances (including, ^{32}P , ^{35}S , ^3H , ^{125}I), fluorescent dyes (including, 5-bromodesoxyuridin, fluorescein, acetylaminofluorene, digoxigenin) or biotin. Preferably, polynucleotides are labeled at their 3' and 5' ends. A label can also be used to capture the primer, so as to facilitate the immobilization of either the primer or a primer extension product, such as amplified DNA, on a solid support. A capture label is attached to the primers or probes and can be a specific binding member which forms a

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binding pair with the solid's phase reagent's specific binding member (e.g. biotin and streptavidin). Therefore depending upon the type of label carried by a polynucleotide or a probe, it may be employed to capture or to detect the target DNA. Further, it will be understood that the polynucleotides, primers or probes provided herein, may, themselves, serve as the capture label.

The probes of the present invention are useful for a number of purposes. They can be notably used in Southern hybridization to genomic DNA. The probes can also be used to detect PCR amplification products. They may also be used to detect mismatches in the EFG gene or mRNA using other techniques.

Any of the polynucleotides, primers and probes of the present invention can be conveniently immobilized on a solid support. Solid supports are known to those skilled in the art. A solid support, as used herein, refers to any material which is insoluble, or can be made insoluble by a subsequent reaction. The solid support can be chosen for its intrinsic ability to attract and immobilize the capture reagent. Alternatively, the solid phase can retain an additional receptor which has the ability to attract and immobilize the capture reagent. The additional receptor can include a charged substance that is oppositely charged with respect to the capture reagent itself or to a charged substance conjugated to the capture reagent. As yet another alternative, the receptor molecule can be any specific binding member which is immobilized upon (attached to) the solid support and which has the ability to immobilize the capture reagent through a specific binding reaction. The receptor molecule enables the indirect binding of the capture reagent to a solid support material before the performance of the assay or during the performance of the assay. The solid phase thus can be a plastic, derivatized plastic, magnetic or non-magnetic metal, glass or silicon surface of a test tube, microtiter well, sheet, bead, microparticle, chip, sheep (or other suitable animal's) red blood cells, duracytes and other configurations known to those of ordinary skill in the art. The polynucleotides of the invention can be attached to or immobilized on a solid support individually or in groups of at least 2, 5, 8, 10, 12, 15, 20, or 25 distinct polynucleotides of the invention to a single solid support. In addition, polynucleotides other than those of the invention may be attached to the same solid support as one or more polynucleotides of the invention.

Consequently, the invention also comprises a method for detecting the presence of a

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nucleic acid comprising a nucleotide sequence of SEQ ID N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116, 120,124,128,132,136,140,144,148,152,156,160,164,168, a fragment or a variant thereof and a complementary sequence thereto in a sample, said method comprising the following

5 steps of:

a) bringing into contact a nucleic acid probe or a plurality of nucleic acid probes which can hybridize with a nucleotide sequence included in a nucleic acid sequence of SEQ ID

10 N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116, 120,124,128,132,136,140,144,148,152,156,160,164,168, a fragment or a variant thereof and a complementary sequence thereto and the sample to be assayed; and

b) detecting the hybrid complex formed between the probe and a nucleic acid in the sample.

Any polynucleotide provided herein may be attached in overlapping areas or at
15 random locations on a solid support. Alternatively the polynucleotides of the invention may be attached in an ordered array wherein each polynucleotide is attached to a distinct region of the solid support which does not overlap with the attachment site of any other polynucleotide. Preferably, such an ordered array of polynucleotides is designed to be "addressable" where the distinct locations are recorded and can be accessed as part of an
20 assay procedure. Addressable polynucleotide arrays typically comprise a plurality of different oligonucleotide probes that are coupled to a surface of a substrate in different known locations. The knowledge of the precise location of each polynucleotides location makes these "addressable" arrays particularly useful in hybridization assays. Any addressable array technology known in the art can be employed with the polynucleotides
25 of the invention. One particular embodiment of these polynucleotide arrays is known as the Genechips, and has been generally described in US Patent 5,143,854; PCT publications WO 90/15070 and 92/10092.

II. EFG Polypeptides and Anti-EFG Antibodies

30 One aspect of the invention pertains to isolated EFG proteins, and biologically active portions thereof, as well as polypeptide fragments suitable for use as immunogens

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to raise fungus, preferably *Aspergillus*, most preferably *A. fumigatus*, anti-EFG antibodies. In one embodiment, native EFG proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, EFG proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, a EFG protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the EFG protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of EFG protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of EFG protein having less than about 30% (by dry weight) of non-EFG protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-EFG protein, still more preferably less than about 10% of non-EFG protein, and most preferably less than about 5% non-EFG protein. When the EFG protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, i.e., culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

The term "polypeptide" refers to a polymer of amino acids without regard to the length of the polymer; thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide. This term also does not specify or exclude post-expression modifications of polypeptides, for example, polypeptides which include the covalent attachment of glycosyl groups, acetyl groups, phosphate groups, lipid groups and the like are expressly encompassed by the term polypeptide. Also included within the definition are polypeptides which contain one or more analogs of an amino acid (including, for example, non-naturally occurring amino acids, amino acids which only occur naturally in an unrelated biological system, modified amino acids from mammalian systems etc.), polypeptides with substituted linkages, as well as other modifications known in the art,

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both naturally occurring and non-naturally occurring.

The term "recombinant polypeptide" is used herein to refer to polypeptides that have been artificially designed and which comprise at least two polypeptide sequences that are not found as contiguous polypeptide sequences in their initial natural
5 environment, or to refer to polypeptides which have been expressed from a recombinant polynucleotide.

Biologically active portions of a EFG protein include peptides comprising amino acid sequences sufficiently homologous to or derived from an amino acid sequence of the EFG protein having a sequence of SEQ ID
10 N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118, 122,126,130,134,138,142,146,150,154,158,162,166,170, which include less amino acids than the full length EFG proteins, and exhibit at least one activity of a EFG protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the EFG protein. A biologically active portion of a EFG protein can be a
15 polypeptide which is, for example at least 15, 25, 50, 100, 150, 200, 300, 400, 500, or more amino acids in length. The upper length just mentioned is of course to be adapted according to the size of the protein.

In a preferred embodiment, the EFG protein comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID
20 N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118, 122,126,130,134,138,142,146,150,154,158,162,166,170. The invention also concerns the polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID
N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116,
25 120,124,128,132,136,140,144,148,152,156,160,164,168, a complementary sequence thereof or a fragment thereto. The present invention embodies isolated, purified, and recombinant polypeptides comprising a contiguous span of at least 6 amino acids, preferably at least 8 to 10 amino acids, more preferably at least 12, 15, 20, 25, 30, 40, 50, 100, 200, 300, 400, 500, 600 or 650 amino acids in length (upper length defined as
30 mentioned above).

In other embodiments, the EFG protein is substantially homologous to SEQ ID

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N^o3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118, 122,126,130,134,138,142,146,150,154,158,162,166,170, and retains the functional activity (at least 50, 60, 80, 90, 99%) of a protein of SEQ ID N^o3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118, 122,126,130,134,138,142,146,150,154,158,162,166,170 yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the EFG protein is a protein which comprises an amino acid sequence at least about 60% homologous to an amino acid sequence of SEQ ID N^o3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118, 122,126,130,134,138,142,146,150,154,158,162,166,170, and retains the functional activity of an EFG proteins of SEQ ID N^o3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118, 122,126,130,134,138,142,146,150,154,158,162,166,170, respectively.

15 Preferably, the protein is at least about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 92%, 95%, 97%, 98%, 99% or 99.8% homologous to a sequence of SEQ ID N^o3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118, 122,126,130,134,138,142,146,150,154,158,162,166,170.

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence and non-homologous sequences can be disregarded for comparison purposes). In a preferred embodiment, the length of a reference sequence aligned for comparison purposes is at least 30%, preferably at least 40%, more preferably at least 50%, even more preferably at least 60%, and even more preferably at least 70%, 80%, 90% or 95% of the length of the reference sequence. The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (i.e., as used herein amino acid or nucleic acid "identity" is equivalent to amino acid or nucleic acid "homology").

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The comparison of sequences and determination of percent homology between two sequences can be accomplished using a mathematical algorithm, preferably the alignment method of Needleman and Wush, J. Mol. Biol., 1970, n°48, p443, using the GAP GCC package (Devereux et al., Nucl. Acid. Res., 1984, vol12, p387). An other non-limiting
5 example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Karlin and Altschul (1990) Proc. Natl. Acad. Sci. USA 87:2264-68, modified as in Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, et al. (1990) J. Mol. Biol. 215:403-10. BLAST nucleotide searches can be
10 performed with the NBLAST program, score=100, wordlength=12 to obtain nucleotide sequences homologous to EFG nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score=50, wordlength=3 to obtain amino acid sequences homologous to EFG protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described
15 in Altschul et al., (1997) Nucleic Acids Research 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See <http://www.ncbi.nlm.nih.gov>. Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, CABIOS (1989). Such an algorithm is
20 incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

The invention also provides EFG chimeric or fusion proteins. As used herein, a
25 EFG "chimeric protein" or "fusion protein" comprises a EFG polypeptide operatively linked, preferably fused in frame, to a non-EFG polypeptide. In a preferred embodiment, a EFG fusion protein comprises at least one biologically active portion of a EFG protein. In another preferred embodiment, a EFG fusion protein comprises at least two biologically active portions of a EFG protein. For example, in one embodiment, the fusion protein is a
30 GST-EFG fusion protein in which the EFG sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant EFG.

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In another embodiment, the fusion protein is a EFG protein containing a heterologous signal sequence at its N-terminus, such as for example to allow for a desired cellular localization in a certain host cell.

The EFG fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject in vivo. Moreover, the EFG-fusion proteins of the invention can be used as immunogens to produce anti-EFG antibodies in a subject, to purify EFG ligands and in screening assays to identify molecules which inhibit the interaction of EFG with a EFG target molecule.

The present invention also pertains to variants of the EFG proteins which function as either EFG mimetics or as EFG inhibitors. Variants of the EFG proteins can be generated by mutagenesis, e.g., discrete point mutation or truncation of a EFG protein. An agonist of the EFG proteins can retain substantially the same, or a subset, of the biological activities of the naturally occurring form of a EFG protein. An antagonist of a EFG protein can inhibit one or more of the activities of the naturally occurring form of the EFG protein by, for example, competitively inhibiting the EFG activity of a EFG protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function.

In a preferred embodiment, variants of a EFG protein which function as EFG antagonists can be identified by screening combinatorial libraries of mutants, e.g., truncation mutants, of a EFG protein for EFG protein antagonist activity. In one embodiment, a variegated library of EFG variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of EFG variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential EFG sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g., for phage display) containing the set of EFG sequences therein. There are a variety of methods which can be used to produce libraries of potential EFG variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the

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sequences encoding the desired set of potential EFG sequences.

In addition, libraries of fragments of a EFG protein coding sequence can be used to generate a variegated population of EFG fragments for screening and subsequent selection of variants of a EFG protein. In one embodiment, a library of coding sequence
5 fragments can be generated by treating a double stranded PCR fragment of a EFG coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease,
10 and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the EFG protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA
15 libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of EFG proteins. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of
20 vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected.

In one embodiment, cell based assays can be exploited to analyze a variegated EFG library.

25 Modified EFG proteins can be used for such purposes as enhancing therapeutic or prophylactic efficacy, or stability (e.g., ex vivo shelf life and resistance to proteolytic degradation in vivo). Such modified peptides, when designed to retain at least one activity of the naturally occurring form of the protein, are considered functional equivalents of the EFG protein described in more detail herein. Such modified peptide can be produced, for
30 instance, by amino acid substitution, deletion, or addition.

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Whether a change in the amino acid sequence of a peptide results in a functional EFG homolog (e.g. functional in the sense that it acts to mimic or antagonize the wild-type form) can be readily determined by assessing the ability of the variant peptide to produce a response in cells in a fashion similar to the wild-type EFG protein or competitively inhibit such a response. Peptides in which more than one replacement has taken place can readily be tested in the same manner.

A wide range of techniques are known in the art for screening gene products of combinatorial libraries made by point mutations, as well as for screening cDNA libraries for gene products having a certain property. Such techniques will be generally adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of EFG proteins. The most widely used techniques for screening large gene libraries typically comprises cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates relatively easy isolation of the vector encoding the gene whose product was detected.

The invention also provides for identification and reduction to functional minimal size of the EFG domains of the subject EFG proteins to generate mimetics, e.g. peptide or non-peptide agents, which are able to disrupt binding of a polypeptide of the present invention with a EFG target protein. Thus, such mutagenic techniques as described above are also useful to map the determinants of EFG proteins which participate in protein-protein interactions involved in, for example, binding to a EFG target protein. To illustrate, the critical residues of a EFG protein which are involved in molecular recognition of the EFG target can be determined and used to generate EFG target-13P-derived peptidomimetics that competitively inhibit binding of the EFG to the EFG target. By employing, for example, scanning mutagenesis to map tile amino acid residues of a particular EFG protein involved in binding a EFG target, peptidomimetic compounds can be generated which mimic those residues in binding to a EFG target, and which, by inhibiting binding of the EFG protein to the EFG target protein, can interfere with the function of a EFG target in transcriptional regulation of one or more genes. For instance, non hydrolyzable peptide analogs of such residues can be generated using retro-inverse peptides (e.g., see U.S. Patents 5,116,947 and 5,219,089; and Pallai et al. (1983) Int J

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Pept Protcin Res 21:84-92), benzodiazepine (e.g., see Freidinger et al. in Peptides: Chemistry and Biology, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), azepine (e.g., see Huffman et al. in Peptides.- Chemistry and Biology, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988).

5 An isolated EFG protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind EFG using standard techniques for polyclonal and monoclonal antibody preparation. Even if they are internal fungus protein, EFG proteins may induce an immunitary response in contact with the host organism.

A full-length EFG protein can be used or, alternatively, the invention provides antigenic peptide fragments of EFG for use as immunogens. The antigenic peptide of EFG
10 comprises at least 8 amino acid residues of an amino acid sequence of SEQ ID N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118, 122,126,130,134,138,142,146,150,154,158,162,166,170, and encompasses an epitope of EFG such that an antibody raised against the peptide forms a specific immune complex
15 with EFG. Preferably, the antigenic peptide comprises at least 10 amino acid residues, more preferably at least 15 amino acid residues, even more preferably at least 20 amino acid residues, and most preferably at least 30 amino acid residues.

Preferred epitopes encompassed by the antigenic peptide are regions of EFG that are located on the surface of the protein, e.g., hydrophilic regions.

20 A EFG immunogen typically is used to prepare antibodies by immunizing a suitable subject, (e.g., rabbit, goat, mouse or other mammal) with the immunogen. An appropriate immunogenic preparation can contain, for example, recombinantly expressed EFG protein or a chemically synthesized EFG polypeptide. The preparation can further include an adjuvant, such as Freund's complete or incomplete adjuvant, or similar
25 immunostimulatory agent. Immunization of a suitable subject with an immunogenic EFG preparation induces a polyclonal anti-EFG antibody response.

Accordingly, another aspect of the invention pertains to anti-EFG antibodies. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen
30 binding site which specifically binds (immunoreacts with) an antigen, such as EFG polypeptides. Examples of immunologically active portions of immunoglobulin

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molecules include F(ab) and F(ab').sub.2 fragments which can be generated by treating the antibody with an enzyme such as pepsin. The invention provides polyclonal and monoclonal antibodies that bind EFG polypeptides. The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody
5 molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of EFG polypeptides. A monoclonal antibody composition thus typically displays a single binding affinity for a particular EFG protein with which it immunoreacts.

The invention concerns antibody compositions, either polyclonal or monoclonal,
10 capable of selectively binding, or selectively bind to an epitope-containing a polypeptide comprising a contiguous span of at least 6 amino acids, preferably at least 8 to 10 amino acids, more preferably at least 12, 15, 20, 25, 30, 40, 50, or 100 amino acids of a sequence of
SEQ ID
N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118,
15 122,126,130,134,138,142,146,150,154,158,162,166,170 (upper length according to the total length of each EFG protein). The invention also concerns a purified or isolated antibody capable of specifically binding to a mutated EFG protein or to a fragment or variant thereof comprising an epitope of the mutated EFG protein

Polyclonal anti-EFG antibodies can be prepared as described above by
20 immunizing a suitable subject with a EFG immunogen. The anti-EFG antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized EFG proteins. If desired, the antibody molecules directed against EFG proteins can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as
25 protein A chromatography to obtain the IgG fraction. At an appropriate time after immunization, e.g., when the anti-EFG antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques.

Any of the many well known protocols used for fusing lymphocytes and
30 immortalized cell lines can be applied for the purpose of generating an anti-EFG monoclonal antibody (see, e.g., G. Galfre et al. (1977) Nature 266:55052; Gefter et al.

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Somatic Cell Genet., cited supra; Lerner, Yale J Biol. Med, cited supra; Kenneth, Monoclonal Antibodies, cited supra). Moreover, the ordinarily skilled worker will appreciate that there are many variations of such methods which also would be useful. Typically, the immortal cell line (e.g., a myeloma cell line) is derived from the same mammalian species as the lymphocytes. For example, murine hybridomas can be made by fusing lymphocytes from a mouse immunized with an immunogenic preparation of the present invention with an immortalized mouse cell line. Preferred immortal cell lines are mouse myeloma cell lines that are sensitive to culture medium containing hypoxanthine, aminopterin and thymidine ("HAT medium"). Any of a number of myeloma cell lines can be used as a fusion partner according to standard techniques, e.g., the P3-NS1/1-Ag4-1, P3-x63-Ag8.653 or Sp2/O-Ag14 myeloma lines. These myeloma lines are available from ATCC.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal anti-EFG antibody can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (e.g., an antibody phage display library) with EFG to thereby isolate immunoglobulin library members that bind EFG genes. Kits for generating and screening phage display libraries are commercially available (e.g., the Pharmacia Recombinant Phage Antibody System, Catalog No. 27-9400-01; and the Stratagene SurfZAP.TM. Phage Display Kit, Catalog No. 240612).

Additionally, recombinant anti-EFG antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art.

An anti-EFG antibody (e.g., monoclonal antibody) can be used to isolate EFG by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-EFG antibody can facilitate the purification of natural EFG from cells and of recombinantly produced EFG expressed in host cells. Moreover, an anti-EFG antibody can be used to detect EFG protein (e.g., in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the EFG protein. Anti-EFG antibodies can be used diagnostically to monitor protein levels in tissue as part of a

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clinical testing procedure, e.g., to, for example, determine the efficacy of a given treatment regimen.

III. Recombinant Expression Vectors and Host Cells.

5 Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding a EFG protein (or a portion thereof). Vectors may have particular use in the preparation of a recombinant protein of the invention.

As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a
10 "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other
15 vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are
20 often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

25 The recombinant expression vectors of the invention comprise a EFG nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression
30 vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the

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nucleotide sequence (e.g., in an in vitro transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Such regulatory sequences are described, for example, in

5 Goeddel; Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, Calif. (1990), the disclosure of which is incorporated herein by reference in its entirety. Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences).

10 It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (e.g., EFG proteins,

15 mutant forms of EFG proteins, fusion proteins, or fragments of any of the preceding proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of EFG proteins in prokaryotic or eukaryotic cells. For example, EFG proteins can be expressed in bacterial cells such as *E. coli*, insect cells (using baculovirus

20 expression vectors) yeast cells, or mammalian cells. Suitable host cells are discussed further in Goeddel, Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, Calif. (1990), the disclosure of which is incorporated herein by reference in its entirety. Alternatively, the recombinant expression vector can be transcribed and translated in vitro, for example using T7 promoter regulatory sequences

25 and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion

30 vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of

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the recombinant protein by acting as a ligand in affinity purification. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D. B. and Johnson, K. S. (1988) Gene 67:31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.), the disclosures of which are incorporated herein by
5 reference in their entirety, which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Purified fusion proteins can be utilized in EFG activity assays, (e.g., direct assays or competitive assays, or to generate antibodies specific for EFG proteins, for example.

The invention further provides a recombinant expression vector comprising a
10 DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to EFG mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous
15 expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high
20 efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. et al., Antisense RNA as a molecular tool for genetic analysis, Reviews--Trends in Genetics, Vol. 1(1) 1986, the disclosure of which is incorporated herein by reference in its entirety.

25 Of course, in the present invention, antisense vectors are particularly useful for inhibiting EFG genes expression, most preferably *A.fumigatus* EFG genes.

Antisense constructs may be designed to bind to the promoter and other control regions, exons, introns or even exon-intron boundaries of a gene. Antisense RNA constructs, or DNA encoding such antisense RNAs, may be employed to inhibit gene transcription or
30 translation or both within a host cell, either in vitro or in vivo, such as within a host animal, including a human subject.

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Although shorter oligomers are easier to make and increase in vivo accessibility, numerous other factors are involved in determining the specificity of hybridization. Both binding affinity and sequence specificity of an oligonucleotide to its complementary target increases with increasing length. It is contemplated that oligonucleotides of 8, 9,
5 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more base pairs will be used. One can readily determine whether a given antisense nucleic acid is effective at targeting of the corresponding host cell gene simply by testing the constructs in vitro to determine whether the endogenous gene's function is affected or whether the expression of related genes having complementary sequences is affected.

10 Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such term refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either
15 mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, a EFG protein can be expressed in bacterial cells such as E. coli, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells or human cells).

20 Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques, that can be found in Sambrook, et al. (Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989, the disclosure of which is incorporated herein by reference in its entirety), and other laboratory manuals.

25 For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (e.g., resistance to antibiotics) is generally introduced into the host cells along with the gene of interest.

30 A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (i.e., express) a EFG protein. Accordingly, the invention

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further provides methods for producing a EFG protein using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a EFG protein has been introduced) in a suitable medium such that a EFG protein is produced. In another
5 embodiment, the method further comprises isolating a EFG protein from the medium or the host cell.

In another embodiment, the invention encompasses providing a cell capable of expressing a EFG protein, culturing said cell in a suitable medium such that a EFG protein is produced, and isolating or purifying the EFG protein from the medium or cell.

10 In certain indications, it may be desirable to activate transcription at specific times after administration of the gene therapy vector. This may be done with such promoters as those that are hormone or cytokine regulatable.

IV. Drug screening assays.

15 The invention provides a method (also referred to herein as a "screening assay") for identifying inhibitors, i.e., candidate or test compounds or agents (e.g., preferably small molecules, but also peptides, peptidomimetics or other drugs) which bind to EFG proteins, have an inhibitory effect on, for example, EFG expression or preferably EFG activity, or have an inhibitory effect on, for example, the activity of an EFG target
20 molecule. Assays may be cell based or non-cell based assays. Drug screening assays may be binding assays or more preferentially functional assays.

In preferred embodiments, an assay is a cell-based assay in which a cell which expresses a EFG protein or biologically active portion thereof is contacted with a test compound and the ability of the test compound to inhibit EFG activity determined.
25 Determining the ability of the test compound to inhibit EFG activity can be accomplished by monitoring the bioactivity of the EFG protein or biologically active portion thereof.

The invention further encompasses compounds capable of inhibiting EFG activity. Inhibiting EFG activity refers to the inhibition of EFG gene expression such that fungus growth is inhibited. Preferably, a EFG inhibitor is a selective EFG inhibitor.

30 In a preferred embodiment, an inhibitor is capable of inhibiting EFG activity of at least one EFG protein of SEQ ID

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N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,118, 122,126,130,134,138,142,146,150,154,158,162,166,170, or a fragment or a variant thereof as previously described. Compounds will be assayed for the activities indicated in Table 1 and Table 1bis.

- 5 For instance, the following standard enzymatic tests are appropriated : ATP dependant RNA helicase, guanylate kinase, RNA synthetase, SAM decarboxylase, protein kinase, ferro-chelataze.

Assays are made by using compounds already known to have an effect on the activity tested. For instance compounds known to inhibit protein kinase activity will be tested.

- 10 In one embodiment, the invention provides assays for screening candidate or test compounds which are target molecules of a EFG protein or polypeptide or biologically active portion thereof. In another embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of a EFG protein or polypeptide or biologically active portion thereof. The test compounds of the
15 present invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library approach is used
20 with peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K. S. (1997) Anticancer Drug Des. 12:145).

- Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt et al. (1993) Proc. Natl. Acad. Sci. U.S.A. 90:6909; Erb et al.
25 (1994) Proc. Natl. Acad. Sci. USA 91:11422; Zuckermann et al. (1994). J. Med. Chem. 37:2678; Cho et al. (1993) Science 261:1303; Carrell et al. (1994) Angew. Chem. Int. Ed. Engl. 33:2059; Carell et al. (1994) Angew. Chem. Int. Ed. Engl. 33:2061; and in Gallop et al. (1994) J. Med. Chem. 37:1233.

- Libraries of compounds may be presented in solution (e.g., Houghten (1992)
30 Biotechniques 13:412-421), or on beads (Lam (1991) Nature 354:82-84), chips (Fodor (1993) Nature 364:555-556), bacteria (Ladner U.S. Pat. No. 5,223,409), spores (Ladner

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U.S. Pat. No. '409), plasmids (Cull et al. (1992) Proc Natl Acad Sci USA 89:1865-1869) or on phage (Scott and Smith (1990) Science 249:386-390); (Devin (1990) Science 249:404-406); (Cwirla et al. (1990) Proc. Natl. Acad. Sci. 87:6378-6382); (Felici (1991) J. Mol. Biol. 222:301-310); (Ladner supra.).

5 Determining the ability of the test compound to inhibit EFG activity can also be accomplished, for example, by coupling the EFG protein or biologically active portion thereof with a radioisotope or enzymatic label such that binding of the EFG protein or biologically active portion thereof to its cognate target molecule can be determined by detecting the labeled EFG protein or biologically active portion thereof in a complex. For
10 example, compounds (e.g., EFG protein or biologically active portion thereof) can be labeled with .sup.125 I, .sup.35 S, .sup.14 C, or .sup.3 H, either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, compounds can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label
15 detected by determination of conversion of an appropriate substrate to product.

It is also within the scope of this invention to determine the ability of a compound (e.g., EFG protein or biologically active portion thereof) to interact with its cognate target molecule without the labeling of any of the interactants. For example, a microphysiometer can be used to detect the interaction of a compound with its cognate target molecule
20 without the labeling of either the compound or the receptor. McConnell, H. M. *et al.* (1992) Science 257:1906-1912. A microphysiometer such as a cytosensor is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indicator of the interaction between compound and receptor.

25 In a preferred embodiment, the assay comprises contacting a cell which expresses a EFG protein or biologically active portion thereof, with a target molecule to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to inhibit the activity of the EFG protein or biologically active portion thereof, wherein determining the ability of the test compound to inhibit the
30 activity of the EFG protein or biologically active portion thereof, comprises determining the ability of the test compound to inhibit a biological activity of the EFG expressing cell

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(e.g., determining the ability of the test compound to inhibit transduction or protein:protein interactions).

In another preferred embodiment, the assay comprises contacting a cell which is responsive to a EFG protein or biologically active portion thereof, with a EFG protein or
5 biologically-active portion thereof, to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to modulate the activity of the EFG protein or biologically active portion thereof, wherein determining the ability of the test compound to modulate the activity of the EFG protein or biologically active portion thereof comprises determining the ability of the test compound to modulate
10 a biological activity of the EFG gene-responsive cell (e.g., determining the ability of the test compound to modulate signal transduction or protein:protein interactions).

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a EFG target molecule with a test compound and determining the ability of the test compound to modulate (e.g. stimulate or inhibit) the activity of the EFG target
15 molecule. Determining the ability of the test compound to modulate the activity of a EFG target molecule can be accomplished, for example, by determining the ability of the EFG protein to bind to or interact with the EFG target molecule.

Determining the ability of the EFG protein to bind to or interact with a EFG target molecule can be accomplished by one of the methods described above for determining
20 direct binding. In a preferred embodiment, determining the ability of the EFG protein to bind to or interact with a EFG target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target, detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the induction
25 of a reporter gene (comprising a target-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, e.g., luciferase), or detecting a target-regulated cellular response, for example, signal transduction or protein:protein interactions.

In yet another embodiment, an assay of the present invention is a cell-free assay in
30 which a EFG protein or biologically active portion thereof is contacted with a test compound and the ability of the test compound to bind to the EFG protein or biologically

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active portion thereof is determined. Binding of the test compound to the EFG protein can be determined either directly or indirectly as described above. In a preferred embodiment, the assay includes contacting the EFG protein or biologically active portion thereof with a known compound which binds EFG (e.g., a EFG target molecule) to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a EFG protein, wherein determining the ability of the test compound to interact with a EFG protein comprises determining the ability of the test compound to preferentially bind to EFG or biologically active portion thereof as compared to the known compound.

10 In another embodiment, the assay is a cell-free assay in which a EFG protein or biologically active portion thereof is contacted with a test compound and the ability of the test compound to modulate (preferably inhibit) the activity of the EFG protein or biologically active portion thereof is determined. Determining the ability of the test compound to modulate the activity of a EFG protein can be accomplished, for example, by determining the ability of the EFG protein to bind to a EFG target molecule by one of the methods described above for determining direct binding. Determining the ability of the EFG protein to bind to a EFG target molecule can also be accomplished using a technology such as real-time Biomolecular Interaction Analysis (BIA). Sjolander, S. and Urbaniczky, C. (1991) Anal. Chem. 63:2338-2345 and Szabo et al. (1995) Curr. Opin. Struct. Biol. 5:699-705. As used herein, "BIA" is a technology for studying biospecific interactions in real time, without labeling any of the interactants (e.g., BIAcore). Changes in the optical phenomenon of surface plasmon resonance (SPR) can be used as an indication of real-time reactions between biological molecules.

25 In an alternative embodiment, determining the ability of the test compound to modulate the activity of a EFG protein can be accomplished by determining the ability of the EFG protein to further modulate the activity of a downstream effector (e.g., a growth factor mediated signal transduction pathway component) of a EFG target molecule. For example, the activity of the effector molecule on an appropriate target can be determined or the binding of the effector to an appropriate target can be determined as previously described.

30 In yet another embodiment, the cell-free assay involves contacting a EFG protein

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or biologically active portion thereof with a known compound which binds the EFG protein to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with the EFG protein, wherein determining the ability of the test compound to interact with the EFG protein comprises
5 determining the ability of the EFG protein to preferentially bind to or modulate the activity of a EFG target molecule.

The cell-free assays of the present invention are amenable to use of both soluble and/or membrane-bound forms of isolated proteins (e.g. EFG proteins or biologically active portions thereof or molecules to which EFG targets bind). In the case of cell-free
10 assays in which a membrane-bound form an isolated protein is used it may be desirable to utilize a solubilizing agent such that the membrane-bound form of the isolated protein is maintained in solution.

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either EFG or its target molecule to facilitate
15 separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to a EFG protein, or interaction of a EFG protein with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtitre plates, test tubes,
20 and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided which adds a domain that allows one or both of the proteins to be bound to a matrix. For example, glutathione-S-transferase/EFG fusion proteins or glutathione-S-transferase/target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, Mo.) or glutathione derivatized microtitre plates, which are
25 then combined with the test compound or the test compound and either the non-adsorbed target protein or EFG protein, and the mixture incubated under conditions conducive to complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the beads or microtitre plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either
30 directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of EFG binding or activity determined using

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standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either a EFG protein or a EFG target molecule can be immobilized utilizing conjugation of biotin and streptavidin.

5 Biotinylated EFG protein or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with EFG protein or target molecules but which do not interfere with binding of the EFG protein to its target

10 molecule can be derivatized to the wells of the plate, and unbound target or EFG protein trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the EFG protein or target molecule, as well as enzyme-linked assays which rely on detecting an enzymatic activity

15 associated with the EFG protein or target molecule.

In another embodiment, modulators of EFG expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of EFG mRNA or protein in the cell is determined. The level of expression of EFG mRNA or protein in the presence of the candidate compound is compared to the level of expression of EFG

20 mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of EFG expression based on this comparison. For example, when expression of EFG mRNA or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of EFG mRNA or protein expression.

25 Alternatively, when expression of EFG mRNA or protein is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of EFG mRNA or protein expression. The level of EFG mRNA or protein expression in the cells can be determined by methods described herein for detecting EFG mRNA or protein.

30 In yet another aspect of the invention, the EFG proteins can be used as "bait proteins" in a two-hybrid assay or three-hybrid assay (see, e.g., U.S. Pat. No. 5,283,317;

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Zervos et al. (1993) Cell 72:223-232).

This invention further pertains to novel agents identified by the above-described screening assays and to processes for producing such agents by use of these assays. Accordingly, in one embodiment, the present invention includes a compound or agent obtainable by a method comprising the steps of any one of the aforementioned screening assays (e.g., cell-based assays or cell-free assays). For example, in one embodiment, the invention includes a compound or agent obtainable by a method comprising contacting a cell which expresses a EFG target molecule with a test compound and the determining the ability of the test compound to bind to, or modulate the activity of, the EFG target molecule. In another embodiment, the invention includes a compound or agent obtainable by a method comprising contacting a cell which expresses a EFG target molecule with a EFG protein or biologically-active portion thereof, to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with, or modulate the activity of, the EFG target molecule. In another embodiment, the invention includes a compound or agent obtainable by a method comprising contacting a EFG protein or biologically active portion thereof with a test compound and determining the ability of the test compound to bind to, or modulate (e.g., stimulate or inhibit) the activity of, the EFG protein or biologically active portion thereof. In yet another embodiment, the present invention included a compound or agent obtainable by a method comprising contacting a EFG protein or biologically active portion thereof with a known compound which binds the EFG protein to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with, or modulate the activity of the EFG protein.

Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (e.g., a EFG modulating agent, an antisense EFG nucleic acid molecule, a EFG-specific antibody, or a EFG-binding partner) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for

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treatments as described herein.

The present invention also pertains to uses of novel agents identified by the above-described screening assays for diagnoses, prognoses, and treatments as described herein. Accordingly, it is within the scope of the present invention to use such agents in the design, formulation, synthesis, manufacture, and/or production of a drug or pharmaceutical composition for use in diagnosis, prognosis, or treatment, as described herein. For example, in one embodiment, the present invention includes a method of synthesizing or producing a drug or pharmaceutical composition by reference to the structure and/or properties of a compound obtainable by one of the above-described screening assays. For example, a drug or pharmaceutical composition can be synthesized based on the structure and/or properties of a compound obtained by a method in which a cell which expresses a EFG target molecule is contacted with a test compound and the ability of the test compound to bind to, or modulate the activity of, the EFG target molecule is determined. In another exemplary embodiment, the present invention includes a method of synthesizing or producing a drug or pharmaceutical composition based on the structure and/or properties of a compound obtainable by a method in which a EFG protein or biologically active portion thereof is contacted with a test compound and the ability of the test compound to bind to, or inhibit the activity of, the EFG protein or biologically active portion thereof is determined.

20

V. Methods of treatment.

EFG inhibitors identified according to the methods in the section titled "Drug Screening Assays" can be further tested for their ability to ameliorate or prevent the pathologies associated to *Aspergillus* fungus, and more particularly to *A.fumigatus*, namely invasive pulmonary aspergillosis.

25

An "individual" treated by the methods of this invention is a vertebrate, particularly a mammal (including model animals of human disease, farm animals, sport animals, and pets), and typically a human.

"Treatment" refers to clinical intervention in an attempt to alter the natural course of the individual being treated, and may be performed either for prophylaxis or during the

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course of clinical pathology. Desirable effects include preventing occurrence or recurrence of disease, alleviation of symptoms, diminishment of any direct or indirect pathological consequences of the disease, such as hyperresponsiveness, inflammation, or necrosis, lowering the rate of disease progression, amelioration or palliation of the disease state, and remission or improved prognosis. The "pathology" associated with a disease condition is anything that compromises the well-being, normal physiology, or quality of life of the affected individual.

Treatment is performed by administering an effective amount of a EFG inhibitor. An "effective amount" is an amount sufficient to effect a beneficial or desired clinical result, and can be administered in one or more doses.

The criteria for assessing response to therapeutic modalities employing the compositions of this invention are dictated by the specific condition, measured according to standard medical procedures appropriate for the condition.

15 VI. Pharmaceutical Compositions.

Compounds capable of inhibiting EFG activity, preferably small molecules but also including peptides, EFG antisense nucleic acid molecules, EFG proteins inhibitors, and anti-EFG antibodies (also referred to herein as "active compounds") of the invention can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise a pharmaceutically acceptable carrier. As used herein the language "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. The use of such media and agents for pharmaceutically active substances is well known in the art.

25 Supplementary active compounds can also be incorporated into the compositions.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, e.g., intravenous, intradermal, subcutaneous, oral (e.g., inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following

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components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL.TM. (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Where the active compound is a protein, peptide or anti-EFG antibody, sterile injectable solutions can be prepared by incorporating the active compound in the required amount in an appropriate solvent with one or a combination of ingredients enumerated

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above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred
5 methods of preparation are vacuum drying and freeze-drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral
10 therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, e.g., a gas such as carbon dioxide, or a nebulizer. Systemic administration can also be by transmucosal or transdermal means.
15 For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active
20 compounds are formulated into ointments, salves, gels, or creams as generally known in the art. Most preferably, active compound is delivered to a subject by intravenous injection.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled
25 release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art, for example, as described in U.S. Pat. No. 4,522,811, or are commercially available.

30 It is especially advantageous to formulate oral or preferably parenteral compositions in dosage unit form for ease of administration and uniformity of dosage.

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Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD50 (the dose lethal to 50% of the population) and the ED50 (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD50/ED50. Compounds which exhibit large therapeutic indices are preferred. While compounds that exhibit toxic side effects may be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC50 (i.e., the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

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VII. Diagnostic and Prognostic Uses

The nucleic acid molecules, proteins, protein homologues, and antibodies described herein can be used in one or more of the following methods: diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenetics; and in drug screening and methods of treatment (e.g., therapeutic and prophylactic) as further described herein.

The invention provides diagnostic and prognostic assays for detecting EFG members, as further described. Also provided are diagnostic and prognostic assays for detecting interactions between EFG members and EFG target molecules.

The isolated nucleic acid molecules of the invention can be used, for example, to detect EFG mRNA (e.g., in a biological sample) or a genetic alteration in a EFG gene, and to modulate a EFG activity, as described further below. The EFG proteins can be used to screen for drugs or compounds which modulate, preferably inhibit EFG activity.

Accordingly one embodiment of the present invention involves a method of use (e.g., a diagnostic assay, prognostic assay, or a prophylactic/therapeutic method of treatment) wherein a molecule of the present invention (e.g., a EFG protein, EFG nucleic acid, or most preferably a EFG inhibitor or activator) is used.

VIII. Fungicidal Compositions.

The invention also deals with fungicidal incorporating at least one compound capable to inhibit fungal growth, by inhibiting EFG genes, in particular in diseases of plants due to phytopathogenic fungi, namely *Botrytis cinerea*, *Mycosphaerella graminicola*, *Stagnospora nodorum*, *Blumeria graminis*, *Colleotrichum lindemuthianum*, *Puccinia graminis*, *Leptosphaeria maculans*, *Fusarium oxysporum*, *Fusarium graminearum*, *Venturia inaequalis*, most preferably fungi of the genus *Magnaporthe*, even most preferably *Magnaporthe grisea*.

The invention thus also provides a method of combating fungi at a locus infested or liable to be infested therewith, which comprises applying to the locus the compound of the invention.

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The invention also provides an agricultural composition comprising the compound of the invention in admixture with an agriculturally acceptable diluent or carrier.

The composition can comprise one or more additional active ingredients, for example compounds known to possess plant-growth regulant, herbicidal, fungicidal (such as metalaxyl, oxadixyl, ofurace, benalaxyl and furalaxyl; cymoxanil; mancozeb; chlorothalonil; folpet; captan; famoxadone; fenamidone; spiroxamine; fluazinam; dimethomorph; strobilurins, such as kresoxim-methyl, azoxystrobin and trifloxystrobin, pyrimethanil, cyprodinil; mepanipyrim; and iprodione), insecticidal or acaricidal properties.

The composition of the invention may include for example a dispersing agent, emulsifying agent or wetting agent. Usually they are in the form of an aqueous concentrate.

The concentration of the active ingredient in the composition of the present invention, as applied to plants is preferably within the range of 0.0001 to 1.0 percent by weight, especially 0.0001 to 0.01 percent by weight. In a primary composition, the amount of active ingredient can vary widely and can be, for example, from 5 to 95 percent by weight of the composition.

In the method of the invention, the compound is generally applied to seeds, plants or their habitat. Thus, the compound can be applied directly to the soil before, at or after drilling so that the presence of active compound in the soil can control the growth of fungi which may attack seeds. When the soil is treated directly the active compound can be applied in any manner which allows it to be intimately mixed with the soil such as by spraying, by broadcasting a solid form of granules, or by applying the active ingredient at the same time as drilling by inserting it in the same drill as the seeds. A suitable application rate is within the range of from 5 to 1000 g per hectare, more preferably from 10 to 500 g per hectare.

Alternatively, the active compound can be applied directly to the plant by, for example, spraying or dusting either at the time when the fungus has begun to appear on the plant or before the appearance of fungus as a protective measure. In both such cases the preferred mode of application is by foliar spraying. It is generally important to obtain

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good control of fungi in the early stages of plant growth as this is the time when the plant can be most severely damaged. The spray or dust can conveniently contain a pre- or post-emergence herbicide if this is thought necessary. Sometimes, it is practicable to treat the roots of a plant before or during planting, for example, by dipping the roots in a suitable liquid or solid composition. When the active compound is applied directly to the plant a suitable rate of application is from 0.025 to 5 kg per hectare, preferably from 0.05 to 1 kg per hectare.

Having generally described this invention, a further understanding can be obtained by reference to certain specific examples which are provided herein for purposes of illustration only, and are not intended to be limiting unless otherwise specified.

Example 1: *A. fumigatus* strain construction.

Media and growth conditions were as follows. *A. fumigatus* strains were propagated at 37°C on complete medium or minimal medium with 0.5 mM of various nitrogen sources (sodium glutamate, ammonium tartrate, sodium nitrate, sodium nitrite and hypoxanthine) (Cove 1966). Uridine and uracil were added at a concentration of 5 mM when appropriate. Liquid cultures used for DNA-mediated transformation and genomic DNA preparation were grown in YG (0.5% Yeast Extract, 2% glucose). DNA-mediated transformation was achieved either on protoplasts as described previously (d'Enfert 1996; Osmani *et al.* 1987) or by electroporation of intact conidia as described (Weidner *et al.* 1998).

A. fumigatus stable diploids appropriate for transposon mutagenesis were obtained using the following procedure. In summary, insertional mutagenesis (Weidner *et al.* 1998) of strain CEA17 has led to the isolation of spore color mutants CEA82 and CEA85. White strain CEA88 and reddish strain CEA94 are chlorate resistant derivatives of CEA82 and CEA85 with uncharacterized mutations in a gene involved in the biosynthesis of the molybdene cofactor (*cnx*) and in the nitrate reductase gene (*niaD*), respectively. Strains CEA125 (*w1, cnx1, pyrG1*) and CEA129 (*r7, niaD2, pyrG1*) were obtained from strains CEA88 and CEA94 by growth on media containing 5-fluoro-orotic acid (1 mg/ml) which selects for *pyrG* mutants. Simultaneous growth of CEA125 and CEA129 on minimal

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medium with nitrate as sole nitrogen source yielded heterokaryons that produced grey-green spores similar to that of *A. fumigatus* haploid wild-type strains. This led to the isolation of the stable diploid strain CEA131 (*w1/+*, *+r7*, *crx1/+*, *+niaD2*, *pyrG1/pyrG1*). A chlorate resistant derivative of CEA131 was identified that was unable to use nitrate as the sole nitrogen source and was defective at both *niaD* alleles. This strain is referred to as CEA153 (*w1/+*, *+r7*, *crx1/+*, *niaD4/niaD2*, *pyrG1/pyrG1*). On minimal medium containing nitrate, spontaneous reversion of the haploid strain CEA113 and the diploid strain CEA153 for nitrate utilization was not observed.

10 **Example 2: *in vivo* transposon mutagenesis in *A. fumigatus*.**

Plasmid pNIL160 has been described³⁰. A 2.2 kb *Bam*HI fragment from *ppyrG* containing the *A. nidulans pyrG* gene was cloned at the *Nhe*I restriction site in *impala160*, yielding pNIpyr. *Nde*I-digested pNIpyr was introduced into genomic DNA of strains CEA113 and CEA153 by electroporation of intact conidia as described¹⁹ yielding the haploid strain CEA165 and the diploid strains CEA225, 226 and 227, respectively. *impala160::pyrG* transposition occurs on minimal medium containing nitrate supplemented with 0.02% Triton X-100 at 37°C for 3 days. Genomic DNA preparation and Southern analysis techniques were essentially performed according to Sambrook *et al.* (1989) and Ausubel *et al.* (1992).

20 Plasmid pNIpyr, a derivative of pNIL160³⁰, carries the *A. nidulans niaD* gene encoding nitrate reductase with a copy of *impala160* inserted 10 bp upstream of the translation initiation codon of *niaD* and modified by the insertion of the *A. nidulans pyrG* gene between the 3'-end of the transposase-encoding gene and the 3' inverted terminal repeat. pNIpyr was introduced in *A. fumigatus* strain CEA153, a stable *pyrG*, *niaD* diploid strain, heterozygous for spore color markers. Because of the insertion of *impala160::pyrG* into the *niaD* promoter, the *niaD* allele carried by pNIpyr is not functional. However, when diploid transformants were grown on selective minimal medium with nitrate as sole nitrogen source, *pyrG*⁺, *NiaD*⁺ revertants were observed at a frequency of 10⁻⁵-10⁻⁶. Southern analysis showed that these transformants have only one copy of

30 *impala160::pyrG* integrated into their genome and that all the revertants resulted of *impala* transposition events from the *niaD* promoter to an apparent random site located

elsewhere in the *A. fumigatus* genome (Fig. 2). Sequence analysis of the *niaD* promoter region in all revertants revealed a footprint of usually 5 bp associated with *impala* excision. Characterization of integration targets by sequencing and comparison to public genomic sequences (Tables 1 and 1bis, and data not shown) revealed that the transposition of *impala160::pyrG* in *A. fumigatus* 1) occurs at a genomic TA dinucleotide which is duplicated during the integration process; 2) is apparently random without sequence preference (except the TA dinucleotide); and 3) is not associated with genomic rearrangements. All of these characteristics are typical for transposition of the *Tc1-mariner* family members and was previously observed for *impala160* transposition events in *F. oxysporum*²⁸, *A. nidulans*²⁹ and *M. grisea*³⁰. Therefore, *impala* appears as the most suitable tool to generate random tagged mutation in *A. fumigatus* since insertional mutagenesis through DNA-mediated transformation results in various types of rearrangements of the transforming and genomic DNA.

Example 3: parasexual genetic screening.

Haploidization of *A. fumigatus* diploid strains was conducted on selective haploidization medium [complete medium containing 1.2 µg/ml benomyl (ALDRICH, 10 mg/ml in DMSO)] or on non-selective haploidization medium (selective haploidization medium plus uridine and uracil) for 5 days at 37°C. Haploid progenies are easily identified by the production of white and reddish-colored sectors after haploidization of grey-green diploid strains.

Three diploid transformants (namely *A. fumigatus* CEA225, CEA226 and CEA227) were used to generate a collection of random diploid heterozygous revertants. Haploidization of heterozygous strains was induced by the destabilizing reagent benomyl and results from mitotic chromosomal non-disjunction^{18,31}. Since each revertant has a single mutated chromosomal locus tagged by *impala160::pyrG*, parasexual genetics on selective and non-selective haploidization media permits to distinguish insertions that occur in non-essential versus essential chromosomal targets (Fig. 1). Strains CEA225, CEA226, CEA227 and 97% of 2,386 revertants showed no difference on selective and non-selective haploidization media after two independent tests, indicating that integration of pNIpyr into the genome of the parental transformants and integration of *impala160::pyrG*

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in the diploid revertants had not occurred into an essential chromosomal region. On selective haploidization medium, 73 revertants (3%) did not yield haploid conidia as evidenced by the absence of colored sectors (Fig. 3). Diploid strains of *A. fumigatus* are hypersensitive to benomyl and only haploid strains can grow at the benomyl concentration used³¹. However, the transient formation of aneuploids leads to the formation of a cal on selective haploidization medium that potentially over-grow haploid strains with morphological defects. To identify mutants which could have been selected in our screening because of the slow growth of haploid progenies rather than the lethality of the insertion, ca. 10⁶ haploid progenies obtained on non-selective haploidization medium were tested for the presence of *impala160::pyrG* by growth on selective medium. Twenty nine diploid revertants (29/2,386 = 1.2%) never yielded haploid pyrG⁺ progenies and were defined as carrying an integration of *impala160::pyrG* into a chromosomal locus essential for *A. fumigatus* growth.

Example 4A: sequence determination.

Genomic sequences bordering *impala160::pyrG* are determined by an adaptation of a two-step PCR strategy developed by Chun *et al.*³⁶ and using transposon specific primers. More precisely concerning the two step PCR, first, ca. 100 ng of genomic DNA were amplified in 50 µl using oligonucleotides ppyr1 and PCRall or ppyr3 and PCRall (4 pmol/µl final) and the following amplification protocol: a denaturation step at 94°C for 3 min. followed by 5 cycles of the following steps: denaturation at 94°C for 30 sec, annealing at 35°C for 30 sec, extension at 72°C for 1 min, and 30 cycles of the following steps: denaturation at 94°C for 30 sec, annealing at 45°C for 30 sec, extension at 72°C for 1 min. A last elongation step was done at 72°C for 3 min. Final concentrations for MgCl₂ and dNTPs were 3 mM and 0.2 mM, respectively. One microliter of the PCR reaction was subjected to a second amplification using similar reaction conditions and oligonucleotides ppyr2 and PCRa12N (if ppyr1 and PCRall had been used in the first reaction) or ppyr4 and PCRa12N (if ppyr3 and PCRall had been used in the first reaction). The following amplification protocol was used: 30 cycles of the following steps: denaturation at 94°C for 30 sec, annealing at 60°C for 30 sec, extension at 72°C for 1 min. A last elongation step was done at 72°C for 3 min. In some instances,

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- oligonucleotides PCRa13, PCRa14, and PCRa15 were used in place of PCRall. PCR products were separated by electrophoresis on a 2% TBE-agarose gel and major PCR products were purified with the Qiaquick Gel Purification Kit (Qiagen, France) according to the supplier's instructions. Purified PCR products are sequenced using ppyr2 or ppyr4 as primers (ESGS, Evry, France). Nucleotide sequences obtained in this manner and trimmed for ppyrG sequences are compared using blastx or blastn (Altschul *et al.* 1990) to protein databases and to the preliminary sequence data of the *A. fumigatus* genome project which were obtained from The Institute for Genomic Research (TIGR) website (<http://www.tigr.org>).
- More precisely concerning the transposon specific primers, two primers were used [primers Imp1: ATGAAGGCGTAAGTTCCTTGC (SEQ ID No.61) and Imp2: GTGTGGAGGAAGAAAGAGC (SEQ ID No.62)]. Sequencing reactions were performed by ESGS (Evry, France) with the primer Imp2 directly on the major PCR product purified from agarose gel using the Qiaquick gel extraction kit (QIAGEN). After elimination of transposon sequences, genomic tags were compared to the *A. fumigatus* TIGR genomic data (www.tigr.org). Results present in this study were obtained from the sequence release of November 14, 2001. At this time, the shotgun sequencing of *A. fumigatus* progressed to 6X sequence coverage (28.7 Mb in 1,578 assemblies of over 1,000 bp in size). From TIGR data, specific primers were designed and used in standard PCR reactions and confirmed the absence of genomic rearrangements after transposon integration and the presence of a wild type chromosomal locus in each of the diploid revertants tested.

Table 2. Primer sequences

ppyr1 (5'end)	GGAAGACGGGCAGTTAGTCC (SEQ ID No.63)
ppyr3 (3'end)	CCCAGGCTTTACACTTATGC (SEQ ID No.64)
PCRa1 1	GGCCACGCGTCGACTAGTAG(N) ₁₀ GATAT (SEQ ID No.65)
PCRa1 3	GGCCACGCGTCGACTAGTAC(N) ₁₀ ACGTC (SEQ ID No.66)
PCRa1 4	GGCCACGCGTCGACTAGTAC(N) ₁₀ TGGAC (SEQ ID No.67)
PCRa1 5	GGCCACGCGTCGACTAGTAC(N) ₁₀ ACGTG (SEQ ID No.68)
ppyr2N (5'end)	CGAAGTTGACGTTTCAGTATGC (SEQ ID No.69)

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ppyr4N (3'end)	TGACCATGATTACGCCAAGC (SEQ ID No.70)
PCRal 2N	GGCCACGCGTCGACTAGTAC (SEQ ID No.71)

Ppyr primers are specific of the ppyrG plasmid used for insertional mutagenesis. The pentamer at the 5' end of the random primer (PCRal, 3, 4 and 5) is expected to bind once in a kb. It is chosen according to the GC% of *A. fumigatus* (ca.50%) and does not occur
5 in the region of ppyrG located between ppyr primers and the linearized plasmid end.

Example 4B: characterization of *A. fumigatus* essential genes.

Genomic sequences bordering *impala160::pyrG* were obtained for 21 of the 29 diploid strains mentioned above. Except for one strain (4-1-3), corresponding genomic regions
10 were identified (Table 1 and Table 1bis) in the public preliminary sequence data of the *A. fumigatus* genome available at The Institute for Genomic Research (<http://www.tigr.org>). Similarity searches of the NCBI non-redundant sequence database performed using the BLASTx algorithm³² identified three main categories of insertional mutants (Tables 1 and 1bis). The first category includes 15 strains that have an insertion of
15 *impala160::pyrG* into genes with homologues in other fungal species. The second category is composed of three strains with *impala160::pyrG* integration occurring into intergenic regions. The last category includes two strains with *impala160::pyrG* integration in genes without homologues in public databases and classified as *A. fumigatus* specific essential genes.

20 In nine of the fifteen strains of the first category, integration of *impala160::pyrG* occurs into homologues of genes demonstrated as essential for *S. cerevisiae* growth (Tables 1 and 1bis). These genes are involved in a broad range of essential biological processes such as protein synthesis (*YGL245W*), protein maturation (*WBP1*) and protein transport (*SRP101*), nuclear architecture (*NAR1*), RNA processing (*DBD10*), nucleotide
25 metabolism (*GUK1*), chromatin structure (*RSC9*) and cell cycle control (*CDC27*). Four additional *impala160::pyrG* integrations occur into genes encoding homologues of non-essential *S. cerevisiae* proteins for which essentiality in *A. fumigatus* is not unexpected: ribosomal proteins *RPL1* and *RPL17* are duplicated in the yeast genome and therefore are not independently essential although the double mutation is lethal; a null mutation of

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MSW1 encoding the yeast tryptophanyl-tRNA synthetase localized in mitochondria leads to a slow growth phenotype; and *S. cerevisiae gos1* null mutant fail to germinate at 37°C, the temperature of the lethality screen.

Two genes encoding homologues of *S. cerevisiae* proteins that are not essential for yeast growth, namely Rim11p and Y11034w (Tables 1 and 1bis), have been identified as essential for *A. fumigatus* growth. These proteins are conserved among lower eukaryotes but their role has not been precisely evaluated yet. Analysis of the Rim11p and its *Schizosaccharomyces pombe* counterpart (*SKP1*) suggest that these protein might be involved in spore formation and for mitosis, although they are not essential for viability in these two species. That the corresponding homologues are essential in *A. fumigatus* might be explained by their implication in additional essential pathways and for discrepancies in the contribution of similar biological pathways to the biology of *A. fumigatus* and other lower eukaryotes.

The second class of mutants includes three revertants in which transposon integration occurs in the vicinity (<200 bp) of the deduced translation initiation codon of three genes which are likely to be essential for *A. fumigatus* growth based to their homology to genes essential for *S. cerevisiae* growth: *RPL14* (revertant 10-304) encodes an essential ribosomal protein and *COX10* (revertant 10-175) and *HEM15* (revertant 11-4-9) are required for heme biosynthesis (Table1). It is likely that *impala* integration prevents proper expression of these three genes but the inventors cannot exclude an additional effect on genes divergently transcribed from these intergenic regions.

Example 5: *impala* transposition characteristics.

The correlation between the parasexual genetics phenotype and the nature of the mutated genes supports the idea that genes genuinely essential for *A. fumigatus* growth can be identified among diploid heterozygous mutants. However, the proportion of *impala160::pyrG* integration in essential genes observed in this study (1.2%) is lower than expected. In *S. cerevisiae*, 17% of the 6,200 genes are essential¹³. Considering a similar frequency of essential genes in *A. fumigatus*, a genome size of 30 Mb with approximately 8000 genes, the inventors have estimated at 8 to 10% the frequency of heterozygous diploids that should have an essential phenotype after parasexual genetics.

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In an attempt to understand the observed lower frequency, the inventors have characterized insertions of *impala160::pyrG* in different contexts. In fourteen diploid revertants not classified as essential but that showed an altered growth pattern on selective haploidization medium only two revertants had an insertion of *impala160::pyrG* in ORFs greater than two kb and these were not similar to known proteins. Interestingly, five *impala160::pyrG* integration (36%) were located 5' (<200 bp) of the deduced translation initiation codon of genes which have homologues in databases, including a tRNA seryl transferase essential in *S. cerevisiae*. In 18 random diploid strains with a non-essential phenotype only one transposon insertion occurred in a protein-coding region, corresponding to the homologue of the non-essential *A. nidulans amdA* gene, while five insertions (28%) were found 5' (<300 bp) of start codons of homologues of non-essential *S. cerevisiae* genes (data not shown). Similar results have been obtained upon analysis of *impala160::pyrG* integrations in a haploid *A. fumigatus* strain (data not shown). These results suggest that *impala160::pyrG* has a tendency to insert preferentially into non-coding regions thus resulting in phenotypically silent mutations as already observed for other transposons³⁴. However, the inventors positive screening by parasexual analysis enrich for insertions that lie predominantly in ORFs.

In summary, through the analysis of 2,364 *A. fumigatus* diploid insertional mutants the inventors have been able to identify 21 previously uncharacterized essential genes (SEQ ID N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,116,120,124,128,132,136,140,144,148,152,156,160,164,168) several of which could not have been predicted as essential for *A. fumigatus* growth based on the knowledge gained from studies in other fungal species. Despite an apparent not truly random distribution of the *impala* element, transposon mutagenesis is a promising tool for insertional mutagenesis in filamentous fungi. A large scale genomic approach is now underway for the systematic identification of essential *A. fumigatus* genes by automatisation of the strategy. This represent an important step for the definition of novel antifungal treatments. Interestingly, the inventors have observed that some heterozygous diploid strains with an integration of *impala* in genes necessary for efficient growth show reduced growth compared to a parental diploid strain (data not shown). In *S. cerevisiae* or *C. albicans*, several

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heterozygous diploids with a mutation in a gene essential for growth also show reduced growth or increased sensitivity to drugs targeting the corresponding gene product^{15,35}. This phenomenon, referred to as haploinsufficiency, can form the basis for the identification of antifungal components that target the product of the mutated gene^{15,35}.

- 5 In order to achieve the results described the inventors used the following experimental protocols:

Example 6: cDNA analysis.

- 10 PCR were carried on DNA prepared from a *A. fumigatus* cDNA library in order to:
- 1) check for expression of a subset of genes identified by transposon;
 - 2) confirm the location of postulated exon/intron splice sites; and
 - 3) identify transcription start sites and polyadenylation sites.
- 15 The *A. fumigatus* cDNA library was obtained from M. Monod (CHUV, Lausanne, Switzerland). It was constructed by InVitrogen using cDNA prepared from *A. fumigatus* strain Y1090 and Lambda gT11 as the cloning vector. Following amplification, DNA of the library was prepared using the Qiagen Lambda Midi Kit.
- 20 PCR were performed on an aliquote of the prepared DNA using standard reaction conditions. PCR used universal primers (Gt11f1, Gt11f3, gt11Rev) corresponding to regions of Lambda flanking the cDNA cloning sites and primers specific to each of the candidate genes.
- 25 PCR primers used herein are listed in Table 3 below:

Table 3. Primer sequences

Oligonucleotide	5'-3' sequence	
10.175.2	GTTGGATCTTTGGGTTCTG	(SEQ ID No.72)
10.304.4	CGCGAATCTGATGACATAGC	(SEQ ID No.73)
10.4.20.2	CTCTTCGCTTCATCGTACCC	(SEQ ID No.74)
11.4.9.4	ATTAGTCCATGCGAGCATCC	(SEQ ID No.75)
11.6.20.2	GCCTGAGCCTAGTCCATCAC	(SEQ ID No.76)
2.1.1.1	CTCGCAGGTCGATTTCACCTC	(SEQ ID No.77)
2.1.1.2	GGAGGAAACCTTGTCACCAC	(SEQ ID No.78)

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Table 3 (continued)

2.1.1.5	TACCGAGAAGGAGGTCATGG	(SEQ ID No.79)
2.1.1.6	TCCAGTCAAGGTTGGTGATG	(SEQ ID No.80)
2.1.1.9	CGAGACCATCCTACCTCAG	(SEQ ID No.81)
4.3.4.2	ACACTCACC GCCTTAACCAC	(SEQ ID No.82)
5.3.11.2	AGTGCCCTTCATTCAGTTCC	(SEQ ID No.83)
6.8.13.2	GCGACTTTGAGGGA ACTATCC	(SEQ ID No.84)
7.5.9.3	CACCACCCACCTTATGAAGC	(SEQ ID No.85)
7.5.9.4	ACCAGGAGAATCAGCGACAC	(SEQ ID No.86)
8.62.2	GGGACGAAGAATACGAGCTG	(SEQ ID No.87)
Gt11f1	CTGAATATCGACGGTTTCC	(SEQ ID No.88)
Gt11f3	GCACATTGGCTGAATATCG	(SEQ ID No.89)
Gt11Rev	TTGACACCAGACCAACTGGTAATG	(SEQ ID No.90)

The oligonucleotides that were used in the different PCR reactions are listed in Table 4 below. PCR products were gel purified using standard procedures and subjected to DNA sequencing using sequencing oligonucleotides as indicated in Table 4 below. Sequencing was performed at GenomeExpress (Grenoble, France) and Sequentia (Clermont-Ferrand, France).

Table 4. Oligonucleotides for PCR and sequencing

Gene id	March 2002	March 2003	PCR	5' oligo.			sequencing oligo.
	ORF SEQ ID	ORF SEQ ID			3' oligo.		
CEA229_genomic	59	97	PCR1	Gt11f3	8.62.2		8.62.2
CEA232_genomic	50	109	PCR2	Gt11f1	10.175.2		10.175
CEA232_genomic	50	109	PCR3	Gt11f1	10.175.2		10.175.2
CEA234_genomic	47	117	PCR4	Gt11f3	10.304.4		10.304.4
CEA257_genomic	17	133	PCR5	2.1.1.1	2.1.1.2		2.1.1.2
CEA257_genomic	17	133	PCR6	2.1.1.5	2.1.1.6		2.1.1.5
CEA257_genomic	17	133	PCR7	2.1.1.9	Gt11Rev		2.1.1.9
CEA257_genomic	17	133	PCR8	Gt11f3	2.1.1.2		2.1.1.2
CEA261_genomic	29	149	PCR9	7.5.9.3	7.5.9.4		7.5.9.3
CEA261_genomic	29	149	PCR10	7.5.9.3	Gt11Rev		7.5.9.3
CEA265_genomic	53	165	PCR11	GT11f1	11.4.9.4		11.4.9.4

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Table 4 (continued)

CEA280_genomic	173	PCR12	Gt11f3	6.8.13.2	6.8.13.2
CEA281.1_genomic/CEA281.2_genomic	177 and 181	PCR13	Gt11f3	5.3.11.2	5.3.11.2
CEA282_genomic	183 and 189	PCR14	GT11f1	10.4.20.2	10.4.20.2
CEA282_genomic	186 and 189	PCR15	GT11f3	10.4.20.2	10.4.20.2
CEA283_genomic		PCR16	GT11f1	11.6.20.2	11.6.20.2
CEA284.1_genomic/CEA284.2_genomic	194 and 198	PCR17	Gt11f1	4.3.4.2	4.3.4.2

Using this approach, we could confirm that sequences of SEQ ID N° 95, 107, 115, 131, 147, 171 are expressed in *A. fumigatus* grown in standard culture medium. Furthermore, the following results could be obtained:

1. PCR1 located the polyadenylation site 189 bp 3' of the proposed stop codon in SEQ ID N°95;
2. PCR3 located the transcription start of SEQ ID N°107, 103 bp 5' of the proposed start codon and confirmed the location of the first intron;
3. PCR4 located the transcription start site of SEQ ID N°115, 113 bp upstream of the proposed start codon, identified an intron in the 5'-untranslated region from position -84 to position -12 relative to the proposed start codon and confirmed the proposed location of the first and second introns;
4. PCR5 and PCR8 confirmed the proposed location of the first intron in SEQ ID N°131;
5. PCR6 confirmed the proposed location of the second and third introns in SEQ ID N°131;
6. PCR 7 located the polyadenylation site 106 bp 3' of the proposed stop codon in SEQ ID N°131;

7. PCR9 and PCR10 confirmed the proposed location of the third intron in SEQ ID N°147 and located two alternative polyadenylation sites 143 bp and 167 bp 3' of the proposed stop codon in SEQ ID N°147.

5 **Example 7: comparison of *A. fumigatus* EFG proteins with proteins of other fungal species.**

EFG proteins of SEQ ID 106 to SEQ ID 174 were systematically compared to the genome of *A. nidulans* using the TBLASTN algorithm, to the genome and gene set of *Magnaporthe grisea* using the TBLASTN algorithm and to the protein set of *Neurospora crassa* and *Saccharomyces cerevisiae* using the BLASTP algorithm.

10 *A. nidulans* sequence data were obtained from the Aspergillus Sequencing project at the Whitehead Institute for Genome Research (<http://www.genome.wi.mit.edu/annotation/fungi/aspergillus/index.html>). The first release referred to as the Monsanto release was used.

15 *M. grisea* sequence data were obtained from the Magnaporthe Sequencing Project [Ralph Dean, Fungal Genomics Laboratory at North Carolina State University (www.fungalgenomics.ncsu.edu), and Whitehead Institute/MIT Center for Genome Research (www-genome.wi.mit.edu); <http://www-genome.wi.mit.edu/annotation/fungi/magnaporthe/index.html>]. Release 2.1 was used.

20 *N. crassa* sequence data were obtained from the Neurospora Sequencing Project [Whitehead Institute/MIT Center for Genome Research (www-genome.wi.mit.edu); <http://www-genome.wi.mit.edu/annotation/fungi/neurospora/index.html>] Release 3 was used. *S. cerevisiae* sequence data were obtained from the Saccharomyces Genome Database (<http://genome-www.stanford.edu/Saccharomyces/>).

25 *A. nidulans*, *M. grisea*, *N. crassa* and *S. cerevisiae* closest homologues of the *A. fumigatus* EFG proteins were subsequently compared to the genome of *A. fumigatus* using the TBLASTN algorithm and the data available from the *A. fumigatus* genome project (<http://tigrblast.tigr.org/ufmg/>) in order to evaluate whether these proteins are
30 orthologues of the *A. fumigatus* EFG proteins (BDBH = yes) or are only homologues of

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the *A. fumigatus* EFG proteins with an *A. fumigatus* orthologue that differs from the *A. fumigatus* EFG protein (BDBH= no).

Results presented in Table 5 below show that:

- all EFG proteins have a orthologue in the genome of *A. nidulans*
- 5 - two EFG proteins are specific to *Aspergilli* (SEQ ID 98 and SEQ ID 170)
- one EFG protein is specific to filamentous ascomycetes (SEQ ID 174)
- the remaining 18 EFG proteins have orthologues in all investigated species.

Consequently targets might be identified that are specific to *Aspergilli*, to filamentous ascomycetes or that have a broad spectrum. This analysis is reinforced by the comparison
10 that was made to human proteins, whose results are shown in Table 6 below. As expected, SEQ ID 98 and SEQ ID 174 do not have a homologue encoded by the human genome thus defining targets for antifungal drugs that would show limited side effects.

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Table 5

Clone Id	Protein in Id	March 2002 Amino acid SEQ ID	March 2003 Amino acid SEQ ID	S. cerevisiae closest homologue	Protein length (aa)	Probability (e value)	Similarity	BDBH	Essential	A. nidulans homologue	M. grisea homologue	BDBH	N. crassa homologue	BDBH
in S.c.														
10-80	CEA 231 _{prot}	3	106	DBP10/YD L031w	995	e-166	55% on 949 aa	yes	yes	ANI6IC8821 (92% 347 #1-345); ANI6IC3840 (69% 166 #772-934 + 83% 55 #723-777); ANI6IS3472 (83% 129 #471-599 + 92% 14 #600-613); ANI6IS468 (57% 132 #418-547); ANI6IC10656 (74% 313 #1-273 + 77% 270 #307-574)	MG04179.1 (0.0 65% 943)	yes	NCU077 yes 12.1 (0.0 69% 958)	
10-291	CEA 233 _{prot}	6	114	NAR1/YN L240c	491	4E-59	48% on 465 aa	yes	yes		CEA233_homol_ Mgrisea (not in Mgrisea Db; contig 2,226 1621..71)	yes	NCU032 yes 04.1 (e-159 62% 613)	
7-1-19	CEA 254 _{prot}	9	122	GUU1/YD R454c	187	2E-62	81% on 182 aa	yes	yes	ANI6IC9151 (75% 132 #2-110 + 91% 88 #111-198)	MG06764.1 (6e-58 77% 183)	yes	NCU063 yes 00.1 (1e-61 78% 181)	
10-3-7	CEA 255 _{prot}	12	126	SRP10/YD DR292c	621	e-102	62% on 431 aa	yes	yes	ANI6IC10591 (77% 346 #168-513 + 86% 160 #502-658); ANI6IC6709 (80% 149 #1-129)	MG02663.1 (0.0 67% 654)	yes	NCU006 yes 25.1 (e-174 67% 620)	
2-6-4	CEA 256 _{prot}	15	130	WBP1/YE L002c	430	2E-37	46% on 432 aa	yes	yes	ANI6IC5302 (69% 520 #1-460)	MG02821.1 (e-125 66% 465)	yes	NCU006 yes 69.1 (e-128 64% 469)	

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Table 5 (continued)

2-1-1 16 CEA 257 prot	18	134	YGL245w	724	0.0	67% on 622 aa	yes	yes	ANI61C10340 (83% 624 #92-715); ANI61C6256 (82% 62 #1-62)	yes	MG05956.1 (0.0 69% 633)	yes	NCU088 94.1 (0.0 72% 631)
2-10- 16 CEA 258 prot	21	138	CDC27/YB L084c	758	4E-71	63% on 304 aa	yes	yes	ANI61C8961 (84% 402 #390-786 + 55% 229 #171- 399 + 63% 53 #119-171); ANI61C6854 (87% 114 #1- 114)	yes	MG06292.1 (e-174 57% 821)	yes	NCU002 13.1 (e- 173 57% 820)
5-4- 21 CEA 259 prot	24	142	RSC9/YM L127w	581	5E-29	45% on 414 aa	yes	yes	ANI61C10567 (92% 382 #1- 382); ANI61C1244 (81% 144 #425-568)	yes	MG02493.1 (6e-61 51% 470)	yes	NCU038 92.1 (7e- 66 52% 478)
2-10- 21 CEA 260 prot	27	146	SPE2/YOL 052c	396	1E-34	51% on 462 aa	yes	yes	ANI61C9610 (82% 247 #39- 273 + 80% 236 #264-491 + 94% 36 #6-41)	yes	MG10635.1 (e-143 67% 479)	yes	NCU010 83.1 (e- 163 71% 502)
7-5-9 CEA 261 prot	30	150	RPL17A/Y KL180w RPL17B/Y JL177w	136	5E-40	92% on 113 aa	yes	no	ANI61C1126 (96% 70 #50- 119 + 77% 69 #8-72)	yes	MG04114.1 (3e-57 96% 118)	yes	NCU070 14.1 (3e- 58 86% 139)
10-2- 18 CEA 262 prot	33	154	RPL1A/Y GL135w RPL1B/Y L220w	255	9E-86	86% on 238 aa	yes	no	ANI61C3974 (96% 170 #43- 212 + 94% 50 #207-256)	yes	MG06919.1 (e-116 93% 238)	yes	NCU014 52.1 (e- 114 91% 241)
9-11 CEA 230 prot	36	102	MSW1/YD R268w	379	2E-26	43% on 154 aa	yes	no	ANI61C6741 (79% 130 #249-398 + 84% 93 #53-145 + 56% 140 #137-249)	yes	MG00474.1 (6e-85 64% 351)	yes	NCU001 13.1 (e- 101 67% 374)

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Table 5 (continued)

4-3-3 CEA 263 prot	39	158	GOS17YH L031c	223	8E-31	60% on 224 aa	yes	no	ANI61C8624 (93% 172 #56- 227 + 91% 38 #23-60)	yes	MG04454.1 (5e-71 76% 226)	yes	NCU027 06.1 (7e- 74 78% 224)
11-6- CEA 11 264 prot	42	162	RIM11/Y MR139w	370	e-104	77% on 323 aa	no	no	ANI61C8742 (74% 246 #16- 217 + 87% 33 #215-247 + 93% 15 #1-15); ANI61C11836 (79% 108 #263-350 + 88% 44 #351- 394)	yes	MG03972.1 (0.0 93% 394)	yes	NCU041 85.1 (0.0 92% 394)
8-47 CEA 228 prot	45	94	YFL034w	1074	5E-42	60% on 248 aa	no	no	ANI61C7512 (75% 306 #374-679); ANI61C7189 (49% 225 #1-217)	yes	MG08873.1 (1e-69 73% 240)	yes	NCU016 72.1 (2e- 89 50% 631)
10- CEA 304 234 prot	48	118	RPL14A/Y HL001w RPL14B/Y KL006w	138	1E-24	63% on 130 aa	yes	no	ANI61C6709 (90% 90 #43- 132 + 79% 55 #1-55)	yes	MG02659.1 (3e-40 70% 132)	yes	NCU006 34.1 (5e- 35 38% 132)
10- CEA 175 232 prot	51	110	HEM15/Y ORI76w	393	e-112	71% on 352 aa	yes	yes	ANI61C8249 (94% 200 #79- 278 + 56% 132 #1-132)	yes	MG01513.1 (e-172 78% 420)	yes	NCU082 91.1 (e- 175 79% 422)
11-4- CEA 9 265 prot	54	166	COX10YYP L172c	462	1E-45	43% on 341 aa	yes	no	ANI61C1412 (50% 301 #20- 320)	yes	MG05944.1 (2e-79 52% 351)	yes	NCU061 41.1 (6e- 81 51% 351)

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Table 5 (continued)

2-10-18	CEA 266- prot	57	170	no hit found			AN161C1220 (57% 305 #233-537)	yes	MG00013.1 (9 e- 06 39% 254)	no	NCU055 88.1 (2e- 07 37% 289)	no
8-62	CEA 229- prot	60	98	no hit found			AN161C3462 (72% 472 #237-707 + 68% 59 #710- 768); AN161C1809 (63% 179 #762-926); AN161C9531 (80% 97 #7- 103)	yes	no hit found	ND	ND no hit found	ND
6-8-13	CEA 280- prot		174	no hit found			AN161C5802 (68% 182 #15- 190)	yes	MG04487.1 (6e-11 45% 175)	yes	NCU099 96.1 (1e- 11 46% 175)	yes
5-3-11	CEA 281- 1 _{pr} at		178	PAC2/TER 007w	518	8.4 e-14 50% fragmented	AN161C7709 (76% 206 #280-482 + 74% 146 #60- 205 + 98% 53 #6-58)	yes	MG00378.1 (2e-95 51% 641)	yes	NCU091 39.1 (2e- 98 50% 634)	yes
5-3-11	CEA 281- 2 _{pr} at		182	no hit found			AN161C868 (72% 169 #47- 211)	yes	MG07998.1 (2e-48 52% 300)	yes	NCU040 32.1 (5e- 42 48% 335)	yes
10-4-20	CEA 282- 1 _{pr} at		186	PBP2/TER 233w	413	2.1 e-26 50% fragmented	AN161C4164 (79% 205 #1- 200 + 82% 158 171-328); AN161C6387 (55% 142 #323-464)	yes	MG00514.1 (e-125 60% 485)	yes	NCU092 37.1 (e- 131 60% 492)	yes
10-4-20	CEA 282- 2 _{pr} at		190	SEC3/TER 008c	1337	2.2 e-03 44% on 277 aa	AN161C11139 (67% 281 #54-344); AN161C4164 (71% 60 #1-60)	yes	MG00515.1 (2e-41 50% 315)	yes	NCU092 38.1 (4e- 36 65% 334)	yes

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Table 5 (continued)

4-3-4 CEA 284 1 _{pr} α	195	EMAS7DR 038c	1091	2.5 e-260	65% fragmented	yes	no	AN161C1006 (88% 336 #429-760 + 86% 260 H167- 426 + 78% 190 H1-169); AN161C1748 (84% 212 #851-1039 + 95% 73 #781- 853) AN161C8195 (39% 126 #232-330); AN161C1069 (63% 56 #335-90)	yes	MG10730.1 (0.0 72% 1072)	yes	NCU050 46.1 (0.0 74% 1038)
4-3-4 CEA 284 2 _{pr} α	199	no hit found							yes	MG10932.1 (2e-08 40% 117)	no	NCU007 23.1 (3e- 07 37% 106)

Table 6

Clone Id	Protein Id	March 2002 Amino acid SEQ ID	March 2003 Amino acid SEQ ID	Nearest human homologue at the integration of site <i>imp160::pyrG</i>	Probability	Protein Length (aa)	Identity (%)	Similarity (%)	Human protein Ref
10-80	CEA231 ₋ prot	3	106	ATP-dependent RNA helicase	e-123	882	261/594 (43%)	353/594 (58%)	NP_07697
10-291	CEA233 ₋ prot	6	114	protein related to Narf	4E-59	476	168/474 (35%)	216/474 (45%)	NP_07193
7-1-19	CEA254 ₋ prot	9	122	guanylate kinase 1	5E-52	197	98/179 (54%)	131/179 (72%)	NP_00084
10-3-7	CEA255 ₋ prot	12	126	signal recognition particle receptor	1E-88	638	232/668 (34%)	334/668 (49%)	NP_00313

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Table 6 (continued)

2-6-4	CEA256_	15	130	dolichyl-diphosphooligosaccharide- protein glycosyltransferase	4E-45	456	124/423 (29%)	213/423 (50%)	NP_00520
2-1-1	CEA257_	18	134	glutamyl-prolyl tRNA synthetase	e-135	1440	260/614 (42%)	372/614 (60%)	NP_00443
2-10-16	CEA258_	21	138	cell division cycle protein 27	5E-81	824	168/465 (36%)	257/465 (55%)	NP_00124
5-4-21	CEA259_	24	142	zinc finger protein of the cerebellum 2	0.001	532	28/102 (27%)	37/102 (35%)	NP_00906
2-10-21	CEA260_	27	146	S-adenosylmethionine decarboxylase 1	5E-50	334	140/447 (31%)	215/447 (47%)	NP_00162
7-5-9	CEA261_	30	150	ribosomal protein S17; 40S ribosomal protein	1E-36	135	85/119 (71%)	98/119 (81%)	NP_00101
10-2-18	CEA262_	33	154	ribosomal protein S3a; 40S ribosomal protein	1E-76	264	151/246 (61%)	190/246 (76%)	NP_00099
9-11	CEA230_	36	102	tryptophanyl tRNA synthetase 2 (mitochondrial)	7E-27	360	64/183 (34%)	104/183 (55%)	NP_05665
4-3-3	CEA263_	39	158	golgi SNAP receptor complex member 1; Golgi SNARE	6E-21	250	67/247 (27%)	125/247 (50%)	NP_00486
11-6-11	CEA264_	42	162	glycogen synthase kinase 3 beta	e-137	433	241/352 (68%)	281/352 (79%)	NP_00208
8-47	CEA228_	45	94	hypothetical protein	6E-28	421	69/188 (36%)	100/188 (52%)	4.2 CAB39107
8-62	CEA229_	60	98	no hit found					
6-8-13	CEA280_		174	no hit found					

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Table 6 (continued)

5-3- 11	CEA281. 1_prot	178					108/199 (54%)	91/211 (43%)	NP_00318 4.1
5-3- 11	CEA281. 2_prot	182				5E-29	75/199 (37%) 55/211 (26%)		NP_00911 8.1
10-4- 20	CEA282. 1_prot	186				0.020	22/64 (34%)	36/64 (56%)	
10-4- 20	CEA282. 2_prot	190				1E-14	59/194 (30%)	96/194 (49%)	NP_00618 7.1
4-3-4	CEA284. 2_prot	199							

beta-tubulin cofactor E
WW domain-containing binding
protein 4; formin binding protein 21
poly(rC) binding protein 1;
heterogenous nuclear
ribonucleoprotein X
no hit found
no hit found

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REFERENCES

1. Latgé, J. P. *Aspergillus fumigatus* and aspergillosis. *Clin Microbiol Rev* 12, 310-350 (1999).
- 5 2. Latgé, J. The pathobiology of *Aspergillus fumigatus*. *Trends Microbiol* 9, 382-389 (2001).
3. Lin, S., Schranz, J. & Teutsch, S. Aspergillosis case-fatality rate: systematic review of the literature. *Clin Infect Dis* 32, 358-366. (2001).
4. McNeil, M. M. *et al.* Trends in mortality due to invasive mycotic diseases in
10 the United States, 1980-1997. *Clin Infect Dis* 33, 641-647. (2001).
5. Georgopapadakou, N. H. Antifungals: mechanism of action and resistance, established and novel drugs. *Curr Opin Microbiol* 1, 547-557 (1998).
6. Tkacz, J. S. & DiDomenico, B. Antifungals: what's in the pipeline. *Curr Opin Microbiol* 4, 540-545. (2001).
- 15 7. Walsh, T. J. *et al.* New targets and delivery systems for antifungal therapy. *Med Mycol* 38, 335-347. (2000).
8. Groll, A. H., De Lucca, A. J. & Walsh, T. J. Emerging targets for the development of novel antifungal therapeutics. *Trends Microbiol* 6, 117-124 (1998).
9. Perfect, J. R. Fungal virulence genes as targets for antifungal chemotherapy.
20 *Antimicrob Agents Chemother* 40, 1577-1583 (1996).
10. Brown, J. S. *et al.* Signature-tagged and directed mutagenesis identify PABA synthetase as essential for *Aspergillus fumigatus* pathogenicity. *Mol Microbiol* 36, 1371-1380. (2000).
11. Reich, K. A. The search for essential genes. *Res Microbiol* 151, 319-324
25 (2000).
12. Odds, F. C., Gow, N. A. & Brown, A. J. Fungal virulence studies come of age. *Genome Biol* 2 (2001).
13. Winzeler, E. A. *et al.* Functional characterization of the *S. cerevisiae* genome by gene deletion and parallel analysis. *Science* 285, 901-906 (1999).

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PCT/IB03/01374

14. Vidan, S. & Snyder, M. Large-scale mutagenesis: yeast genetics in the genome era. *Curr Opin Biotechnol* 12, 28-34. (2001).
15. De Backer, M. D. *et al.* An antisense-based functional genomics approach for identification of genes critical for growth of *Candida albicans*. *Nat Biotechnol* 19,
5 235-241. (2001).
16. Brookman, J. L. & Denning, D. W. Molecular genetics in *Aspergillus fumigatus*. *Curr Opin Microbiol* 3, 468-474. (2000).
17. Timberlake, W. E. in *More Gene Manipulations in Fungi* (eds. Bennett, J. W. & Lasure, L. L.) 51-85 (Academic Press Inc., Oxford, 1991).
- 10 18. Clutterbuck, A. J. Sexual and parasexual genetics of *Aspergillus* species. *Biotechnology* 23, 3-18 (1992).
19. Brown, J. S., Aufauvre-Brown, A. & Holden, D. W. Insertional mutagenesis of *Aspergillus fumigatus*. *Mol Gen Genet* 259, 327-335 (1998).
- 20 20. d'Enfert, C., Weidner, G., Mol, P. C. & Brakhage, A. A. Transformation systems of *Aspergillus fumigatus*. New tools to investigate fungal virulence. *Contrib Microbiol* 2, 149-166 (1999).
21. Judson, N. & Mekalanos, J. J. Transposon-based approaches to identify essential bacterial genes. *Trends Microbiol* 8, 521-526. (2000).
22. Judson, N. & Mekalanos, J. J. TnAraOut, a transposon-based approach to
20 identify and characterize essential bacterial genes. *Nat Biotechnol* 18, 740-745. (2000).
23. Kumar, A. & Snyder, M. Emerging technologies in yeast genomics. *Nat Rev Genet* 2, 302-312. (2001).
24. Ross-Macdonald, P. *et al.* Large-scale analysis of the yeast genome by
25 transposon tagging and gene disruption. *Nature* 402, 413-418 (1999).
25. Hamer, L. *et al.* Gene discovery and gene function assignment in filamentous fungi. *Proc Natl Acad Sci USA* 98, 5110-5115. (2001).
26. Brown, J. S. & Holden, D. W. Insertional mutagenesis of pathogenic fungi. *Curr Opin Microbiol* 1, 390-394 (1998).

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PCT/IB03/01374

27. Langin, T., Capy, P. & Daboussi, M. J. The transposable element impala, a fungal member of the Tc1-mariner superfamily. *Mol Gen Genet* 246, 19-28 (1995).
28. Hua-Van, A., Pamphile, J. A., Langin, T. & Daboussi, M. J. Transposition of autonomous and engineered impala transposons in *Fusarium oxysporum* and a related species. *Mol Gen Genet* 264, 724-731. (2001).
29. Li Destri Nicosia, M. G. *et al.* Heterologous transposition in *Aspergillus nidulans*. *Mol Microbiol* 39, 1330-1344. (2001).
30. Villalba, F., Lebrun, M. H., Hua-Van, A., Daboussi, M. J. & Grosjean-Courmoyer, M. C. Transposon impala, a novel tool for gene tagging in the rice blast fungus *Magnaporthe grisea*. *Mol Plant Microbe Interact* 14, 308-315. (2001).
31. Hastie, A. C. Benlate-induced Instability of *Aspergillus* diploids. *Nature* 226, 771 (1970).
32. Altschul, S. F. *et al.* Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res* 25, 3389-3402. (1997).
33. Akerley, B. J. *et al.* A genome-scale analysis for identification of genes required for growth or survival of *Haemophilus influenzae*. *Proc Natl Acad Sci U S A* 99, 966-971. (2002).
34. Craig, N. L. Target site selection in transposition. *Annu Rev Biochem* 66, 437-474 (1997).
35. Giaever, G. *et al.* Genomic profiling of drug sensitivities via induced haploinsufficiency. *Nat Genet* 21, 278-283 (1999).
36. Chun, K. T., Edenberg, H. J., Kelley, M. R. & Goebel, M. G. Rapid amplification of uncharacterized transposon-tagged DNA sequences from genomic DNA. *Yeast* 13, 233-240 (1997).
37. Bouchara, J.P. *et al.* The search for virulence determinants in *Aspergillus fumigatus*; *Trends Microbiol.* 3(8), 327-330 (1995).
38. Langfelder, K. *et al.* Identification of a polyketide Synthase Genes (pKsP) of *Aspergillus fumigatus* involved in conidial pigment biosynthesis and virulence. *Med Microbiol Immunol (Berl.)* 187(2), 79-89 (1998).

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39. Tsai, H.F. *et al.* A developmentally regulated gene cluster involved in conidial pigment biosynthesis in *Aspergillus fumigatus*. J. Bacteriol 181(20), 6469-6477 (1999).

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CLAIMS

1. A nucleic acid encoding an Essential For Growth (EFG) polypeptide selected
5 from the group consisting of :
- (i) a nucleic acid molecule encoding a polypeptide comprising the amino acid
sequence depicted in one of SEQ ID
N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,
118,122,126,130,134,138,142,146,150,154,158,162,166,170 ;
- 10 (ii) a nucleic acid molecule comprising the nucleic acid sequence as depicted
in one of SEQ ID
N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,
116,120,124,128,132,136,140,144,148,152,156,160,164,168 ;
- (iii) a nucleic sequence having at least 80, 85, 90, 95, 98, 99% identity with a
15 sequence of SEQ ID
N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,
116,120,124,128,132,136,140,144,148,152,156,160,164,168 ;
- (iv) a nucleic acid molecule which hybridizes under stringent conditions to:
- (a) a nucleic acid as defined in (i), (ii) and (iii), or
- 20 (b) a complementary strand of (a) ;
- (v) a nucleic acid the sequence of which is degenerate as a result of the
genetic code to the sequence of a nucleic acid as defined in (i), (ii), (iii) and (iv).
2. An isolated nucleic acid, said nucleic acid comprising a nucleotide sequence
25 encoding:
- i) a EFG polypeptide comprising an amino acid sequence having at least
80% identity to a sequence of SEQ ID
N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,10
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- 6,170; or
- ii) a biologically active fragment of said polypeptide.
3. An isolated nucleic acid, said nucleic acid comprising a nucleotide sequence
5 encoding:
- i) a EFG polypeptide comprising an amino acid sequence which is
orthologous to a sequence of SEQ ID
N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,10
2,106,110,114,118,122,126,130,134,138,142,146,150,154,158,162,16
10 6,170; or
- ii) a biologically active fragment of said polypeptide.
4. A nucleic acid sequence of any of claims 1 to 3 encoding a polypeptide of
A. fumigatus exhibiting a biological function associated to fungal growth, said
15 nucleic acid comprising a sequence of SEQ ID
N°2,5,8,14,17,20,23,26,29,32,35,38,41,44,47,50,53,56,59,93,97,101,105,109,113,11
7,121,125,129,133,137,141,145,149,153,157,161,165,169.
5. A nucleic acid sequence of claim 4, wherein said biological function
20 associated to fungal growth is chosen among: protein synthesis, protein maturation,
protein transport, nuclear architecture, RNA processing, nucleotide metabolism,
chromatine structure, cell cycle control.
6. The nucleic acid of claim 1, wherein said nucleic acid is operably linked to a
25 promoter.
7. An expression cassette comprising the nucleic acid of claim 6.
8. A host cell comprising the expression cassette of claim 7.

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9. A biologically active polypeptide encoded by a nucleic acid according to any of claims 1 to 5.

10. A polypeptide according to claim 9 or a biologically active fragment thereof,
5 said polypeptide comprising an amino acid sequence of at least 80% amino acid
sequence identity to a sequence of SEQ ID
N°3,6,9,12,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,94,98,102,106,110,114,
118,122,126,130,134,138,142,146,150,154,158,162,166,170.

10 11. A method of identifying a candidate inhibitor of EFG polypeptide, said
method comprising :
a) contacting a EFG polypeptide according to claim 9 or 10 with a test compound ;
b) determining whether said compound selectively binds to said polypeptide, said
binding indicating that said compound is a candidate inhibitor.

15 12. A method of identifying a candidate inhibitor of EFG polypeptide, said
method comprising :
a) contacting said polypeptide with a test compound ;
b) determining whether said compound selectively inhibits the activity of said
20 polypeptide, said inhibition indicating that said compound is a candidate inhibitor.

13. A method for detecting the presence of a nucleic acid comprising a nucleotide
sequence of SEQ ID
N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,
25 116,120,124,128,132,136,140,144,148,152,156,160,164,168, a fragment or a variant
thereof and a complementary sequence thereto in a sample, said method comprising
the following steps of:
a) bringing into contact a nucleic acid probe or a plurality of nucleic acid
probes which can hybridize with a nucleotide sequence included in a nucleic acid

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sequence of SEQ ID
N°1,4,7,10,13,16,19,22,25,28,31,34,37,40,43,46,49,52,55,58,92,96,100,104,108,112,
116,120,124,128,132,136,140,144,148,152,156,160,164,168, a fragment or a variant
thereof and a complementary sequence thereto and the sample to be assayed; and

- 5 b) detecting the hybrid complex formed between the probe and a nucleic acid in
the sample.

14. A method for locating at least one gene essential for the growth of a haploid
fungus, said method comprising the following successive steps :

- 10 - generation of diploid strain from fungal haploid strain ;
 - mutagenesis of said diploid strain;
 - haploidisation of the diploid transformant strain, in selection conditions such
that the absence of haploid progeny is indicative of mutagenesis occurring in
essential gene;

15 wherein said mutagenesis is an *in vivo* transposon mutagenesis.

15. The method of claim 14, wherein said fungus is of the *Aspergillus* genus, or
the *Penicillium* genus.

20 16. The method of claim 14 or 15, wherein said fungus is *Aspergillus fumigatus*.

17. The method of claim 14, wherein the transposon is carried by the plasmid
pNIpyr.

25 18. The method of claim 14 or 17, wherein the transposon is the *impala160*
transposon or a derivative thereof.

19. The method of claim 14, wherein said diploid strain is chosen from the group
comprising CEA 225, CEA 226, and CEA 227.

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20. The method of claim 14, wherein the selection medium is a benomyl-containing medium.
- 5 21. Plasmid pNlpyr (CNCM I-2815).
22. The diploid strain CEA 225 (CNCM I-2816).
23. The diploid strain CEA 226 (CNCM I-2817).
- 10 24. The diploid strain CEA 227 (CNCM I-2818).
25. A method for screening compounds that are active against *A. fumigatus* comprising :
- 15 - preparing an *A. fumigatus* strain that is heterozygous for an EFG gene (heterozygous EFGn/efgn) ;
- preparing an *A. fumigatus* strain that is homozygous for the EFG gene (homozygous EFGn/EFGn) ;
- comparing the effect of a candidate compound on the heterozygous
- 20 EFGn/efgn and on the homozygous EFGn/EFGn,
- the higher inhibiting effect on the heterozygous EFGn/efgn than on the homozygous EFGn/EFGn indicating that the compound is an inhibitor.
26. An isolated nucleic acid sequence according to any of claims 1 to 5,
- 25 obtainable by a method according to claim 14.
27. A composition capable of inhibiting haploid fungal growth, wherein said composition comprises at least one compound capable of inhibiting the expression of at least one EFG gene as defined in any of claims 1 to 5.

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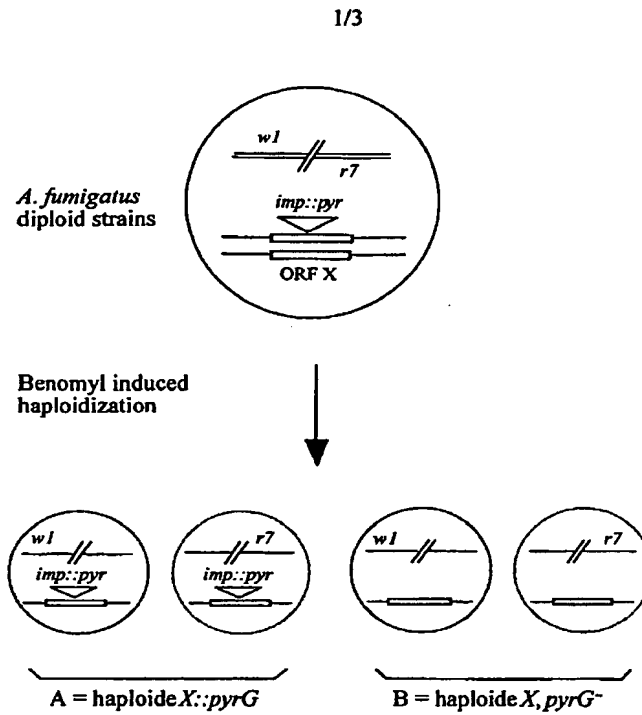
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28. The composition of claim 27, which is a pharmaceutical composition.

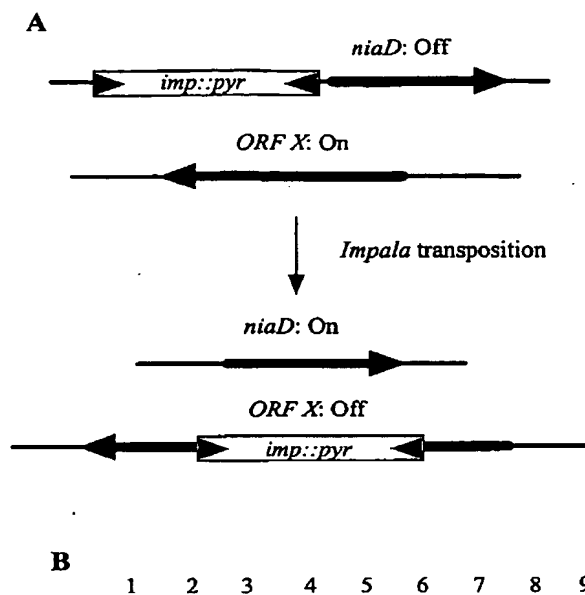
29. The composition of claim 27 or 28, which is a fungicidal composition.

Fig.1



ORF X	Haploid strains	Non selective haploidization	Selective haploidization
Essential gene	A	- Growth	- No growth
	B	+	-
Non essential gene	A	+	+
	B	+	-

Fig.2



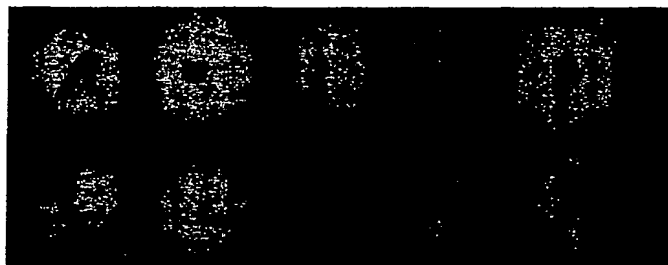
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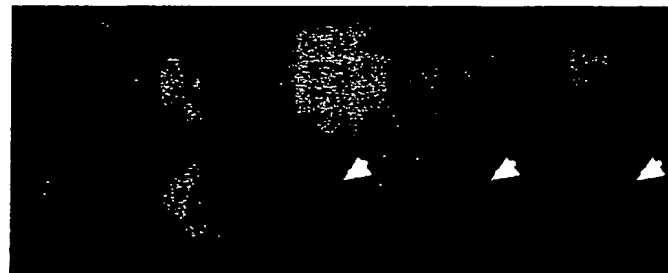
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Fig. 3

A)



B)



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SEQUENCE LISTING

DT09 Rec'd PCT/PTO 13 SEP 2004

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<120> Mutagenesis of Aspergillus fungi and genes essential for growth

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<213> *Aspergillus fumigatus*

<400> 4

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<210> 5

<211> 1592

<212> DNA

<213> *Aspergillus fumigatus*

<400> 5

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cctcaagtca ggcgagctt ggcagccaca tacggaatca ccgagcggga ggcgaaatat 360
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<211> 530

<212> PRT

<213> *Aspergillus fumigatus*

<400> 6

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Gln Ser Glu Asn Pro Tyr Glu Val Thr Lys Glu Asp Lys Val Gln Pro
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Glu Asn Leu Pro Pro Ala Gln Ile Ser Leu Thr Asp Cys Leu Ala Cys
      50             55             60

Ser Gly Cys Val Thr Ser Ala Glu Ala Val Leu Ile Ser Leu Gln Ser
      65             70             75             80

His Thr Glu Val Leu Asn Thr Leu Asp Ser Asp Gly Arg Ile Phe Val
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Ala Ser Val Ser Pro Gln Val Arg Ala Ser Leu Ala Ala Thr Tyr Gly
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Ile Thr Glu Arg Glu Ala Lys Tyr Met Ile Asp Gln Phe Leu Met Gly
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Pro His Gly Leu Arg Ala Gly Gly Lys His Gly Asn Gly Phe Thr Trp
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Asp Glu Val Thr Ser Ser Leu Leu Ser Thr Gly Ser Gly Ser Leu Pro
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 Glu Lys Thr His Pro Phe Ile Leu Pro His Leu Ser Arg Leu Lys Ser
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 Pro Gln Ala Leu Ser Gly Thr Phe Leu Lys Ser Val Leu Ser Lys Ala
 210 215 220
 Leu Gly Val Pro Pro Ser Gln Ile Trp His Leu Ala Ile Met Pro Cys
 225 230 235 240
 Phe Asp Lys Lys Leu Glu Ala Ser Arg Glu Glu Leu Thr Asp Ile Ala
 245 250 255
 Trp Ala Ser Thr Phe Thr Gln Ser Gln Thr Thr Pro Val Arg Asp Val
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 Asp Cys Val Ile Thr Thr Arg Glu Leu Leu Thr Leu Ala Thr Ala Arg
 275 280 285
 Gly Leu Ser Leu Pro Asn Leu Pro Leu Lys Pro Leu Pro Ala Ser Cys
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 305 310 315 320
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 325 330 335
 His His Val Leu Gln Ile Phe Gln Ala Arg Asn Pro Gly Ser Lys Ile
 340 345 350
 Val Thr Gln Arg Gly Arg Asn Ala Asp Val Val Glu Tyr Val Leu Met
 355 360 365
 Ser Ser Gly Asp Glu Pro Leu Phe Arg Ala Ala Arg Tyr Tyr Gly Phe
 370 375 380
 Arg Asn Ile Gln Asn Leu Val Arg Lys Leu Lys Pro Ala Arg Val Ser
 385 390 395 400
 Arg Leu Pro Gly Ala Lys Pro Gln Ala Val Ser Ser Ser Ala Asn Arg
 405 410 415
 Arg Gln Pro Met Ser Arg Asn Ala Ala Pro Ala Gly Thr Gly Ala Asp
 420 425 430
 Tyr Ala Tyr Val Glu Val Met Ala Cys Pro Gly Gly Cys Thr Asn Gly
 435 440 445
 Gly Gly Gln Ile Arg Ile Glu Asp Ala Arg Glu Ala Val Pro Asn Ala
 450 455 460
 Leu Lys Glu Thr Ser Thr Glu Thr Pro Val Ala Ala Pro Lys Pro Thr
 465 470 475 480
 Pro His Glu Gln Arg Ala Trp Leu Ala Arg Val Asp Glu Ala Tyr Tyr
 485 490 495
 Ser Ala Asp Ser Asp Ser Glu Gly Ser Val Thr Thr Glu Pro Val Ser

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500

505

510

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Glu Lys
 530

<210> 7
 <211> 942
 <212> DNA
 <213> *Aspergillus fumigatus*

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<210> 8
 <211> 600
 <212> DNA
 <213> *Aspergillus fumigatus*

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<210> 9
 <211> 200
 <212> PRT
 <213> *Aspergillus fumigatus*

<400> 9
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Pro Ser Gly Thr Gly Lys Ser Thr Leu Leu Lys Arg Leu Phe Ala Glu
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 Tyr Pro Asp Thr Phe Asp Leu Ser Val Ser His Thr Thr Arg Ala Pro
 35 40 45
 Arg Pro Gly Glu Glu Asn Gly Arg Glu Tyr Tyr Phe Thr Thr Lys Glu
 50 55 60
 Asp Phe Leu Asp Leu Val Ser Lys Asn Ala Phe Ile Glu His Ala Gln
 65 70 75 80
 Phe Gly Gly Asn Tyr Tyr Gly Thr Thr Val Gln Ala Val Lys Asp Val
 85 90 95
 Ala Gln Lys Gly Lys Ile Cys Val Leu Asp Ile Glu Met Arg Gly Val
 100 105 110
 Lys Gln Val Lys Arg Thr Asp Leu Asp Ala Arg Phe Leu Phe Leu Ala
 115 120 125
 Pro Pro Ser Leu Glu Glu Leu Glu Lys Arg Leu Arg Gly Arg Ala Thr
 130 135 140
 Glu Thr Glu Glu Ser Leu Thr Lys Arg Leu Ala Gln Ala Lys Asn Glu
 145 150 155 160
 Leu Glu Tyr Ala Ala Gln Pro Gly Ser His Asp Lys Ile Val Val Asn
 165 170 175
 Asp Asp Leu Glu Lys Ala Tyr Lys Glu Leu Arg Asp Trp Ile Val Asp
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 Gly Gly Asn Phe Gly Ala Arg Gln
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<210> 10

<211> 2059

<212> DNA

<213> *Aspergillus fumigatus*

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<210> 11

<211> 1923

<212> DNA

<213> *Aspergillus fumigatus*

<400> 11

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 <211> 641
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 <213> Aspergillus fumigatus

<400> 12

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Asn Asp Val Phe Ile Glu Glu Lys Val Arg Ala Gln Asn Gln Ala Ala
      35              40              45

Ser Ser Ala Ala Pro Ile Tyr Lys Lys Glu Lys Tyr Thr Leu Lys Trp
      50              55              60

Lys Gln Val Lys Asp Phe Asn Leu Ile Phe Val Ala Val Tyr Gln Ser
      65              70              75              80

Leu Leu His Leu Gly Trp Ile Asp Lys Leu Leu Asp Asn Val Ser Thr
      85              90              95

Ile Phe Ile Asp Leu Tyr Lys Asp Glu Leu Arg Ser Thr Arg Ala Arg
      100             105             110

Ile Ile Glu Tyr Pro Phe Asp Lys Tyr Phe Asp Gln Gln Val Arg Glu
      115             120             125

Leu Glu Asp Asn Ala Gly Ala Pro Thr Ser Glu Ser Leu Val Val Glu
      130             135             140

Ile Asn Glu Arg Lys Asp Pro Leu Val Ser Ser Asp Asn Gly Gly Pro
      145             150             155             160

Pro Pro Pro Pro Val Pro Val Ala Gln Gly Val Ala Thr Ser Asp Glu
      165             170             175

Gly Ser Pro Pro Gln Thr Pro Asp Leu Ser Arg Ser Ser Thr Pro Ile
      180             185             190

Ser Gly His Leu Leu Thr Ala Lys Gly Gly Pro Ala Gly Arg Ala Ser
      195             200             205

Arg Arg Ala Arg Lys Ala Ala Asn Ala Ser Ala Thr Ala Ser Ser Gly
      210             215             220

Asp Glu Ser Ile Arg Lys Gly Lys Thr Leu Lys Ser Gly Lys Lys Met
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Arg Lys Trp Asp Ala Asp Gly Phe Ala Asp Glu Asp Asp Gly Lys Val
      245             250             255

Leu Asp Tyr Ser Ala Pro Ala Asp Gly Glu Asp Ala Pro Ala Pro Val
      260             265             270

Val Glu Ala Val Ala Gln Glu Ser Trp Gly Arg Arg Thr Gly Lys Gly
      275             280             285

Gln Phe Val Leu Lys Asp Leu Gly Asp Glu Val His Ser Ile Leu Glu

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385						390					395				400
Arg	Lys	Ile	Leu	Thr	Pro	Thr	Ser	Ser	Leu	Asp	Leu	Leu	Arg	Glu	Ile
			405						410					415	
Asp	Ala	Val	Arg	Ser	Pro	Thr	Ser	Lys	Gly	Gln	Ala	Pro	Arg	Pro	Tyr
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Val	Ile	Ser	Ile	Val	Gly	Val	Asn	Gly	Val	Gly	Lys	Ser	Thr	Asn	Leu
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Gly	Lys	Ile	Cys	Tyr	Phe	Leu	Leu	Gln	Asn	Asn	Tyr	Arg	Val	Leu	Ile
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Ala	Ala	Cys	Asp	Thr	Phe	Arg	Ser	Gly	Ala	Val	Glu	Gln	Leu	Arg	Val
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His	Ala	Arg	Asn	Leu	Lys	Glu	Leu	Ser	Thr	Arg	Glu	Asn	Ala	Gly	Glu
			485						490					495	
Val	Glu	Leu	Tyr	Glu	Lys	Gly	Tyr	Gly	Lys	Asp	Ala	Ala	Asn	Val	Ala
			500					505					510		
Lys	Asp	Ala	Val	Glu	Tyr	Gly	Ala	Ala	Asn	His	Phe	Asp	Val	Val	Leu
		515					520					525			
Ile	Asp	Thr	Ala	Gly	Arg	Arg	His	Asn	Asp	Gln	Arg	Leu	Met	Ser	Ser
		530				535					540				
Leu	Glu	Lys	Phe	Ala	Lys	Phe	Ala	Lys	Pro	Asp	Lys	Ile	Phe	Met	Val
545						550					555				560
Gly	Glu	Ala	Leu	Val	Gly	Thr	Asp	Ser	Val	Met	Gln	Ala	Arg	Asn	Phe
			565						570					575	
Asn	Gln	Ala	Phe	Gly	Thr	Gly	Arg	Asn	Leu	Asp	Gly	Phe	Ile	Ile	Ser
			580					585					590		
Lys	Cys	Asp	Thr	Val	Gly	Asp	Met	Val	Gly	Thr	Leu	Val	Ser	Met	Val
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His	Ala	Thr	Gly	Ile	Pro	Ile	Val	Phe	Leu	Gly	Val	Gly	Gln	His	Tyr
	610					615					620				

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Gly Asp Leu Arg Gly Leu Ser Val Pro Trp Ala Val Asn Leu Leu Met
625 630 635 640

Lys

<210> 13
<211> 1564
<212> DNA
<213> *Aspergillus fumigatus*

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aaattatggg ctgacctaga aggtgctcta acctactgaa cttctacgtt aatatgctaa 180
tattaattgg tagctcgagg atataacctc gacttcgaat cccccaagaa tgacaagctc 240
agcctgttcg aactcggaga ccgaggtctac gaccacatgc ttctcctgcc tcccaagtca 300
aagggttagc gttaccctta gacatgtcca tatgtctgc tttgtacatc tcaattgacc 360
tcttgccag gctatggacc ctcccttacc cccaagaata tcattgattt catgaacaag 420
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ctgctattgg agctcgatct ccatctccct gtcgatcggt cctctgtcac cgtcgatcac 540
ttcaactacg atacactttc tgctccgat aagcatgatg ttctgtact ccaccgacca 600
ggcaagttga ggtccgatac caaggctttc tttgatggcg agggcgttgt agcatttccc 660
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<210> 14
<211> 1380
<212> DNA
<213> *Aspergillus fumigatus*

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aaattatggg ctgacctaga aggatataac ctcgacttgc aatcccccaa gaatgacaag 180
ctcagcctgt tcgaactcgg agaccgagtc tacgaccaca tgcttctcct gcctcccaag 240
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ctattggagc tcgatctcca tctccctgtc gatcgttctt ctgtcaccgt cgatcacttc 420
aactacgata cactttctgc ctccgataag catgatgttc tgctactcca ccgaccaggc 480
aagttgaggt ccgataccaa ggctttcttt gatggcgagg gcgtttagc atttcccaga 540
gccgtccccc acaccctggg cgatgcaaac cctctcattg cgcctattct gcgagcgccc 600
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ggtgatggga agcagatgaa gacggtcaac caggaattcg ccaagcagct tactgcgtgg 840
acattcaagg aaaccggagt cctcaaggtc ggaaagatcg agcatcatct ggctgaagat 900
ggtgaaatca ctcccagaaa gctgaaccct aagatctatc gaataaagaa tgaaactgtc 960
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cccgtccgtc gaacagataa cagtacagtt tacagcacac gattcaccac ccccgatcag 1140
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agcgggtgat gggctctgat tgcgggtctg tgggtccgta tcgctggctt cttagtattc 1320
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<210> 15

<211> 460

<212> PRT

<213> *Aspergillus fumigatus*

<400> 15

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  1              5              10              15

```

```

Arg Ala Leu Ser Ser Ser Gly Ser Arg Leu Leu Val Val Leu Glu Asp
      20              25              30

```

```

Ala Thr Glu Lys Glu Leu Tyr Ser Lys Leu Trp Ala Asp Leu Glu Gly
      35              40              45

```

```

Tyr Asn Leu Asp Phe Glu Ser Pro Lys Asn Asp Lys Leu Ser Leu Phe
      50              55              60

```

```

Glu Leu Gly Asp Arg Val Tyr Asp His Met Leu Leu Leu Pro Pro Lys
      65              70              75              80

```

```

Ser Lys Gly Tyr Gly Pro Ser Leu Thr Pro Lys Asn Ile Ile Asp Phe
      85              90              95

```

```

Met Asn Lys Asp Gly Asn Val Leu Leu Ala Leu Ser Gly Lys Ser Thr
      100             105             110

```

```

Thr Ala Ser Ala Ile Ser Ser Leu Leu Leu Glu Leu Asp Leu His Leu
      115             120             125

```

```

Pro Val Asp Arg Ser Ser Val Thr Val Asp His Phe Asn Tyr Asp Thr
      130             135             140

```

```

Leu Ser Ala Ser Asp Lys His Asp Val Leu Leu Leu His Arg Pro Gly
      145             150             155             160

```

```

Lys Leu Arg Ser Asp Thr Lys Ala Phe Phe Asp Gly Glu Gly Val Val
      165             170             175

```

```

Ala Phe Pro Arg Ala Val Pro His Thr Leu Gly Asp Ala Asn Pro Leu
      180             185             190

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```

Ile Ala Pro Ile Leu Arg Ala Pro Ala Thr Ala Tyr Ser Tyr Asn Pro
      195             200             205

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```

Lys Glu Asp Ala Ser Ser Val Glu Asp Val Ala Ala Thr Gly Ser Gln
      210             215             220

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Leu Ala Leu Val Ser Ala Met Gln Ala Arg Asn Ser Ala Arg Phe Thr
 225 230 235 240
 Leu Leu Gly Ser Val Glu Ser Leu Gln Asp Gln Trp Phe Ser Ala Thr
 245 250 255
 Val Lys Ala Pro Gly Asp Gly Lys Gln Met Lys Thr Val Asn Gln Glu
 260 265 270
 Phe Ala Lys Gln Leu Thr Ala Trp Thr Phe Lys Glu Thr Gly Val Leu
 275 280 285
 Lys Val Gly Lys Ile Glu His His Leu Ala Glu Asp Gly Glu Ile Thr
 290 295 300
 Pro Glu Lys Leu Asn Pro Lys Ile Tyr Arg Ile Lys Asn Glu Thr Val
 305 310 315 320
 Phe Ser Ile Glu Leu Ser Glu Tyr Asn Tyr Asp Arg Tyr Ala Pro Phe
 325 330 335
 Glu Val Pro Thr Gly Asp Ala Val Gln Leu Glu Phe Thr Met Leu Ser
 340 345 350
 Pro Phe His Arg Leu Asn Leu Glu Pro Val Arg Arg Thr Asp Asn Ser
 355 360 365
 Thr Val Tyr Ser Thr Arg Phe Thr Thr Pro Asp Gln His Gly Ile Phe
 370 375 380
 Ser Phe Arg Val Asn Tyr Lys Arg Pro Phe Leu Thr Asn Ile Glu Glu
 385 390 395 400
 Lys Leu Glu Val Thr Val Arg His Phe Ala His Asn Glu Tyr Pro Arg
 405 410 415
 Ser Trp Lys Ile Ser Gly Gly Trp Val Trp Ile Ala Gly Leu Trp Ser
 420 425 430
 Val Ile Ala Gly Phe Leu Val Phe Val Val Ala Trp Leu Tyr Ser Ala
 435 440 445
 Pro Ser Ala Ala Ala Leu Asn Thr Lys Lys Thr Gln
 450 455 460

<210> 16

<211> 2376

<212> DNA

<213> Aspergillus fumigatus

<400> 16

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 gaggatactg cggttcttcg tgaaggagac aaggccgtcg tgcaatacac tggagctagc 180
 ggtaatccta tctttggcct tatcaatgct gttcaggaac tccgcaaaga cttccccttc 240
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 ctgataagtg atactaacc tccttttata ggagaatgaa tggctgtctc agttggaagc 360
 atttgctcct ctagatttca aggcccttga ccctgaattg cagcgccctc ataccacct 420

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cctgctgaga tctttcgtcg tccgttacgc tctctcgacg gccgacattg ccctttgggg 480
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gactcggttg ttctatttct tggaggatct gtgccgtgg gccacatcta cactggaggt 600
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<210> 17

<211> 2145

<212> DNA

<213> *Aspergillus fumigatus*

<400> 17

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gaggatactg cggttcttcg tgaaggagac aaggccgtcg tgcaatacac tggagctagc 180
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<210> 18

<211> 715

<212> PRT

<213> *Aspergillus fumigatus*

<400> 18

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Ser Pro Val Ile Ser Ile Thr Tyr Glu Asp Thr Ala Val Leu Arg Glu
      35             40             45

Gly Asp Lys Ala Val Val Gln Tyr Thr Gly Ala Ser Gly Asn Pro Ile
      50             55             60

Phe Gly Leu Ile Asn Ala Val Gln Glu Leu Arg Lys Asp Phe Pro Phe
      65             70             75             80

Leu Asn Ser Lys Asp Glu Lys Leu Glu Asn Glu Trp Leu Ser Gln Leu
      85             90             95

Glu Ala Phe Ala Pro Leu Asp Phe Lys Ala Leu Asp Pro Glu Leu Gln
      100            105            110

Arg Leu Asp Thr His Leu Leu Leu Arg Ser Phe Val Val Gly Tyr Ala
      115            120            125

Leu Ser Thr Ala Asp Ile Ala Leu Trp Gly Ala Ile Arg Gly Asn Arg
      130            135            140

Val Ala Val Ala Ala Ile Lys Lys Gly Ser Leu Val Asn Val Thr Arg
      145            150            155            160

Trp Phe Tyr Phe Leu Glu Asp Leu Cys Pro Trp Ala Thr Ser Thr Leu
      165            170            175

Glu Val Leu Asn Gln Ala Val Arg Glu Lys Lys Ala Ala Lys Ala Lys
      180            185            190

Glu Gly Ala Ser Tyr Asp Ile Ala Leu Leu Asn Thr Glu Lys Gly Val

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225					230					235					240
Gly	Thr	Leu	Leu	Val	Arg	Phe	Asp	Asp	Thr	Asn	Pro	Ser	Asn	Glu	Lys
				245					250					255	
Leu	Glu	Phe	Gln	Asp	Ala	Ile	Ile	Glu	Asp	Leu	Ala	Leu	Met	Gly	Ile
			260					265					270		
Lys	Pro	Asp	Lys	Met	Ser	Tyr	Thr	Ser	Asp	Tyr	Phe	Asp	Glu	Leu	Tyr
		275					280					285			
Gln	Tyr	Ala	Leu	Gln	Ile	Ile	Lys	Asp	Gly	Asn	Ala	Tyr	Ala	Asp	Asp
290						295					300				
Thr	Glu	Lys	Glu	Val	Met	Ala	Glu	Gln	Arg	Met	Asn	Gly	Lys	Pro	Ser
305					310					315					320
Lys	Arg	Arg	Asp	Ala	Ser	Val	Glu	Glu	Asn	Leu	Ala	Arg	Phe	Glu	Glu
				325					330					335	
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			340					345					350		
Met	Ser	Val	Asp	Asn	Pro	Asn	Lys	Ala	Met	Arg	Asp	Pro	Val	Ile	Tyr
		355					360					365			
Arg	Cys	Asn	Pro	Ala	Pro	His	His	Arg	Thr	Gly	Thr	Lys	Trp	Lys	Ile
370						375					380				
Tyr	Pro	Thr	Tyr	Asp	Phe	Ala	Cys	Pro	Ile	Val	Asp	Ser	Ile	Glu	Gly
385					390					395					400
Val	Thr	His	Ala	Leu	Arg	Thr	Ile	Glu	Tyr	Arg	Asp	Arg	Asn	Pro	Gln
				405					410					415	
Tyr	Gln	Trp	Phe	Leu	Asp	Thr	Leu	Lys	Leu	Arg	His	Val	Gln	Ile	Trp
			420					425					430		
Asp	Phe	Ala	Arg	Met	Asn	Phe	Ile	Arg	Thr	Leu	Leu	Ser	Lys	Arg	Lys
		435					440					445			
Leu	Thr	Lys	Leu	Val	Asn	Gln	Gly	Val	Val	Trp	Gly	Trp	Asp	Asp	Pro
						455					460				
Arg	Phe	Pro	Thr	Ile	Arg	Gly	Ile	Arg	Arg	Arg	Gly	Met	Thr	Ile	Pro
465					470					475					480
Ala	Leu	Arg	Glu	Phe	Ile	Leu	Lys	Gln	Gly	Pro	Ser	Lys	Asn	Ile	Thr
				485					490					495	
Asn	Leu	Asp	Trp	Thr	Leu	Ile	Trp	Ala	Thr	Asn	Lys	Lys	Tyr	Ile	Asp
			500					505					510		
Pro	Val	Ala	Pro	Arg	His	Thr	Ala	Ile	Leu	Lys	Lys	Asp	Met	Val	Lys
		515					520					525			

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Ala Ile Val Lys Gly Gly Pro Ala Thr Pro Tyr Thr Glu Glu Lys Pro
530 535 540

Lys His Gly Lys Asn Pro Ala Val Gly Met Lys Lys Val Val Phe Gly
545 550 555 560

Asn Thr Val Ile Phe Asp Gln Lys Asp Ala Lys Ser Phe Lys Gln Asp
565 570 575

Glu Glu Ile Thr Leu Met Ser Trp Gly Asn Ala Ile Val Arg Lys Ile
580 585 590

Glu Thr Asp Pro Thr Ser Gly Ile Val Lys Glu Leu Glu Leu Glu Leu
595 600 605

His Leu Glu Gly Asp Phe Lys Lys Thr Glu Lys Lys Val Thr Trp Leu
610 615 620

Ser Thr Glu Gly Gln Asp Leu Ile Pro Val Glu Leu Val Asp Phe Asp
625 630 635 640

Tyr Leu Leu Asn Lys Asp Thr Leu Gln Glu Asp Asp Val Leu Glu Asp
645 650 655

Val Leu Asn Lys Asn Thr Glu Phe Arg Glu Asp Ala Val Ala Asp Cys
660 665 670

Asn Val Ala Glu Leu Lys Glu Gly Asp Ile Ile Gln Phe Glu Arg Lys
675 680 685

Gly Tyr Tyr Arg Val Asp Arg Ala Tyr Val Pro Gly Lys Pro Ala Val
690 695 700

Leu Phe Asn Ile Pro Thr Gly Lys Thr Gly Lys
705 710 715

<210> 19

<211> 2639

<212> DNA

<213> *Aspergillus fumigatus*

<400> 19

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PCT/IB03/01374

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<212> DNA

<213> *Aspergillus fumigatus*

<400> 20

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<210> 21

<211> 809

<212> PRT

<213> *Aspergillus fumigatus*

<400> 21

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      35              40              45

Leu Ala Leu Cys His Leu Gln Asn Gly Gln Val Lys Ala Ala Tyr Asp
      50              55              60

Tyr Ser Arg Asn Phe Gly Ser Arg Gly Thr His Leu Gly Cys Ser Tyr
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Val Phe Ala Gln Ala Cys Leu Asp Leu Gly Lys Tyr Leu Glu Gly Ile
      85              90              95

Thr Ala Leu Glu Arg Ser Lys Gly Leu Trp Ala Ser Lys Asn His Trp
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      115             120             125

Val Phe Cys Leu Leu Gly Lys Leu Trp His Ala His Lys Asp Ile Asn
      130             135             140

Lys Ala Val Glu Cys Tyr Val Glu Ser Leu Lys Leu Asn Pro Phe Met
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Trp Asp Ala Phe Gln Gly Leu Cys Asp Thr Gly Val Asn Val Arg Val
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Ser Asn Ile Tyr Lys Leu Asn Ser Glu Leu Leu Ala Val Leu Ser Ser
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Ser Pro Gln Ala Asp Ala Glu Pro Ile Ser Asp Lys Ser Ala His Thr

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Ser	Gly	Val	Pro	Ala	Ser	Ile	Val	His	Glu	Gly	Ala	Glu	Thr	Pro
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Gly	Gln	Ser	Ser	Gly	Ser	Asp	Glu	Phe	Arg	Leu	Ala	Asn	Gly	Met
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 Arg Ala Thr Gln Leu Asp Pro Gln Phe Ala Tyr Gly Phe Thr Leu Gln
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 645 650 655
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 690 695 700
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 705 710 715 720
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 Glu Ala Asn Val His Tyr Leu Leu Gly Lys Leu Tyr Lys Met Leu His
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 Asp Lys Ala Asn Ala Ile Lys His Phe Thr Thr Ala Leu Asn Leu Asp
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<210> 22

<211> 1836

<212> DNA

<213> Aspergillus fumigatus

WO 03/076464

PCT/IB03/01374

<400> 22

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<210> 23

<211> 1836

<212> DNA

<213> *Aspergillus fumigatus*

<400> 23

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WO 03/076464

PCT/IB03/01374

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<210> 24

<211> 611

<212> PRT

<213> *Aspergillus fumigatus*

<400> 24

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          20             25             30

Phe Glu Gly Phe Pro Leu Leu Ala Glu Asn Leu Met Ala Lys Ala Leu
          35             40             45

Asp Ile Ser Leu Val Thr Thr Gly Val Lys Trp Glu Leu Gln Tyr Asp
          50             55             60

Val Leu Gln Leu Ser Asp Arg Val Asn Glu Leu Asn Ser Leu His Gly
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Thr Arg Asp Leu Leu Glu Lys Ile Lys Gln Met Pro Val Thr Leu Pro
          85             90             95

Glu Asp Thr Leu Glu Thr Tyr Glu Phe Asn His Leu Leu Arg Asn Val
          100            105            110

Lys Glu Ala Thr Leu Val Leu Arg Asn Met Val Leu Leu Lys Glu Asn
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Ala Tyr Tyr Val Ser Arg Tyr Ala Lys Gly Leu Leu Arg Asp Phe Leu
          130            135            140

Val Ile Met Ile Asn Leu Pro Asn Gln Pro Arg Leu Asn Glu Ile Lys
          145            150            155            160

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          165            170            175

Asp Pro Glu Asp Pro Leu Trp Ile Ser Leu Leu Asn Cys Leu Gly Ser
          180            185            190

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Ser Thr Glu Leu Asp Glu Pro Glu Ala Asn Arg Ala Met Glu Arg Ile
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PCT/IB03/01374

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 Thr Val Phe Val Pro Arg Met Val Ala Leu Leu Thr His Glu Gly Arg
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 Pro Asn Lys Lys Glu Thr Val Leu Gln Glu Glu Lys Val Ala Pro Pro
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 Pro Ser Asp Ile Pro Arg Val Pro Pro Glu Leu Met Lys Glu Leu Met
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 Pro Ala Ala Glu Phe Ile Lys Asn Val Ser Thr Thr Phe Thr Asn Ala
 370 375 380
 Gln Ala Gln Val Ile Asn Gly Pro Gly Ala Ala Thr Lys Phe Ile Ile
 385 390 395 400
 Lys Gly Ile Arg Pro Leu Glu Thr Ala Tyr Thr Phe Glu Gly Phe Pro
 405 410 415
 Tyr Ile Tyr Cys Lys Trp Ala Asp Asn Ser Lys Pro Ser Lys Thr Cys
 420 425 430
 Gln Arg Ala Phe Lys Ser Pro Ala Glu Leu Arg His His Val Phe Thr
 435 440 445
 Glu His Met Asn Leu Lys Pro Thr Glu Thr Pro Gly His Tyr Asn Leu
 450 455 460
 Glu Lys Ala Glu Ser Pro Val His Thr Cys Leu Trp Asp Asn Cys Thr
 465 470 475 480
 Lys Phe Arg Ser Ser Gly Pro Ser Ala Asn Thr Ala Met Val Ala Gly
 485 490 495
 His Val Ser Ala His Leu Pro Glu Glu Arg Ala Pro Asp Ala Glu Pro
 500 505 510
 Pro Thr Ser Lys Arg Ala Val Leu Gln Glu Arg Ile Val Arg Lys Trp
 515 520 525
 Tyr Tyr Leu Asp Thr Pro Val Asn Glu Arg Gly Glu Pro Phe Gly Val
 530 535 540
 Ala Tyr Lys Ala Ala Leu Val Leu Arg Asn Leu Ala Arg Asn Leu Pro

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545									550									555									560
Thr	Gly	Ile	Ala	Pro	Gln	Tyr	Asn	Gly	Leu	Ser	Trp	Lys	Lys	Ala	Val												
				565					570								575										
Phe	Leu	Ser	His	Arg	Pro	Lys	Ile	Ile	Glu	Ala	Trp	Asp	Arg	Asn	Arg												
				580					585								590										
Ser	Leu	Arg	Lys	Glu	Leu	Thr	Glu	Leu	Ile	Met	Val	Ile	Glu	Lys	Glu												
			595				600						605														
Asp	Tyr	Tyr																									
610																											

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<210> 25
<211> 1542
<212> DNA
<213> Aspergillus fumigatus
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<400> 25						
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aattgccagg	tcctctcgat	tgtttcgtca	gaggatgtgg	acgcctacct	gctctccgag	360
ctctagcatgt	tcggtttggcc	tcacaagaact	atcttgaaga	cttgtggtac	caccactctt	420
ctgtctgtgtc	tcaccacgat	ctctgagatt	gcgcgtttgt	ctcgttggett	ccccagttct	480
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gagaacgcca	agcagttcta	cctcggagaat	gccacttccg	ttcgggagaa	ccgttatcgc	900
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gcgctcggaa	ccgtgggtct	tgaagcctgt	ggactttcct	ctgtgtatcc	taaggagaag	1080
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gagcgcgact	gttcatatgc	gtccttttag	accaacgtac	cgcactcgca	gaacggccag	1260
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tacctggccg	ctcgtcggac	cgccaaaatg	gaacatgtgg	agggatatcg	ccgagtggac	1440
cggattgtcc	acgacctctg	cggctatag	cttgtcttcc	gctattatga	acgcctggac	1500
tggaagaagg	gggccctcga	gctggaagag	gagaqatctt	ga		1542

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<210> 26
<211> 1479
<212> DNA
<213> Aspergillus fumigatus
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<400> 26						
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ggtccagaga	aactcttggg	ggtgtggttc	gcgccttcgc	ctcaggaatt	aggtccagcg	180
cagccgcgcg	gtctgaagga	tgttccggag	gagatctgga	aggacatgtt	ggatctcgtc	240
aattgccagg	tcctctcga	tggttcgta	gaagatctgq	acgcctacct	gctctcgaag	300

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```

tctagcatgt tcgtttggcc tcacaaactc atcttgaaga cttgtggtac caccactctt 360
ctgtctggtc tcccacgcat tctcgagatt gccgctttgt tcggtggctt ccccaagtct 420
accgcccctt ctcgcggaat ctccgtcgcc gctgcgccct accgctctt ctacagccgc 480
aagaacttcc tgttccccga ccgccagcgg ggccctcacc gcagctggag agatgaagtg 540
cggactatgg ataagctctt cctcaacggc agcgcctaca tgattggcaa gatgaatggc 600
gagcactggg acttgtacct gactgaacct cataccatgc tcaccccgcc aacgagcccg 660
ggagccaaga ccgagtttac ggaaacggag accaaggctc tcagtgtacc ccagggcgct 720
gctctgcaga ctgattcgga ggatgagact ttggaagtct tgatgaccga cttggatgag 780
gagaacgcca agcagttcta cctcgagaat gccactgccg ttgctggagaa ccgttatcgc 840
aactcaaatt cggagaagag tggccatggt gatgttttca gcaacacttc ctccgatatc 900
agcgattttg actccgacgg aagccaggtt ctgcctccag agttgactac cgagggtcac 960
gcgctcgaaa ccgtggtctc tgaagcctgt ggactttcct ctgtgtatcc taaggagaag 1020
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tacctggccg ctcgctcgac cgccaaaatg gaacatgtgg agggatatcg ccgagtggac 1380
cggattgtcc acgacctcga cggctatgag cttgtcttcc gctattatga acgcctggac 1440
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```

<210> 27

<211> 493

<212> PRT

<213> *Aspergillus fumigatus*

<400> 27

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Met Val Tyr Ile Gly Ile Pro Lys Asn Tyr Thr Ala Ser Pro Ser Ser
  1             5             10             15

```

```

Phe Ala Gly Thr Pro Ser Leu Thr Ile Asn Tyr Glu Ala Thr Gln Asp
      20             25             30

```

```

Leu Asp Ser Thr Asn Ala Phe Glu Gly Pro Glu Lys Leu Leu Glu Val
      35             40             45

```

```

Trp Phe Ala Pro Ser Ala Gln Glu Leu Gly Pro Ala Gln Pro Ala Gly
      50             55             60

```

```

Leu Lys Ala Val Pro Glu Glu Ile Trp Lys Asp Met Leu Asp Leu Val
      65             70             75             80

```

```

Asn Cys Gln Val Leu Ser Ile Val Ser Ser Glu Asp Val Asp Ala Tyr
      85             90             95

```

```

Leu Leu Ser Glu Ser Ser Met Phe Val Trp Pro His Lys Leu Ile Leu
      100            105            110

```

```

Lys Thr Cys Gly Thr Thr Thr Leu Leu Ser Gly Leu Pro Arg Ile Leu
      115            120            125

```

```

Glu Ile Ala Ala Leu Phe Gly Gly Phe Pro Lys Ser Thr Ala Pro Ser
      130            135            140

```

```

Arg Gly Ile Ser Val Ala Ala Ala Pro Tyr Arg Val Phe Tyr Ser Arg
      145            150            155            160

```

```

Lys Asn Phe Leu Phe Pro Asp Arg Gln Arg Gly Pro His Arg Ser Trp
      165            170            175

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Arg Asp Glu Val Arg Thr Met Asp Lys Leu Phe Leu Asn Gly Ser Ala
 180 185 190
 Tyr Met Ile Gly Lys Met Asn Gly Glu His Trp Tyr Leu Tyr Leu Thr
 195 200 205
 Glu Pro His Thr Met Leu Thr Pro Pro Thr Ser Pro Gly Ala Lys Thr
 210 215 220
 Glu Phe Thr Glu Thr Glu Thr Lys Val Leu Ser Val Pro Gln Gly Ala
 225 230 235 240
 Ala Leu Gln Thr Asp Ser Glu Asp Glu Thr Leu Glu Val Leu Met Thr
 245 250 255
 Asp Leu Asp Glu Glu Asn Ala Lys Gln Phe Tyr Leu Glu Asn Ala Thr
 260 265 270
 Ala Val Ala Glu Asn Arg Tyr Arg Asn Ser Asn Ser Glu Lys Ser Gly
 275 280 285
 His Val Asp Val Phe Ser Asn Thr Ser Ser Asp Ile Ser Asp Phe Asp
 290 295 300
 Ser Asp Gly Ser Gln Val Leu Pro Pro Glu Leu Thr Thr Glu Gly His
 305 310 315 320
 Ala Leu Gly Thr Val Val Ser Glu Ala Cys Gly Leu Ser Ser Val Tyr
 325 330 335
 Pro Lys Glu Lys Tyr Pro Asp Ser Arg Ile Asp Ala Tyr Leu Phe Thr
 340 345 350
 Pro Cys Gly Phe Ser Ala Asn Gly Val Ile Pro Pro Pro Glu Gly Lys
 355 360 365
 Ala Gly Thr His Tyr Phe Thr Val His Val Thr Pro Glu Pro His Cys
 370 375 380
 Ser Tyr Ala Ser Phe Glu Thr Asn Val Pro His Ser Gln Asn Gly Gln
 385 390 395 400
 Thr Thr Ala Gly Ile Ile Lys Gln Val Val Asp Ile Phe Lys Pro Gly
 405 410 415
 Arg Phe Ser Val Thr Leu Phe Glu Ala Lys Pro Ala Leu Ser Gln Val
 420 425 430
 Glu Asp Glu Trp Lys Glu Ala Lys Tyr Leu Ala Ala Arg Arg Thr Ala
 435 440 445
 Lys Met Glu His Val Glu Gly Tyr Arg Arg Val Asp Arg Ile Val His
 450 455 460
 Asp Leu Asp Gly Tyr Glu Leu Val Phe Arg Tyr Tyr Glu Arg Leu Asp
 465 470 475 480
 Trp Lys Gly Gly Ala Pro Arg Leu Gly Glu Glu Arg Ser
 485 490

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<210> 28
 <211> 637
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 28
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 tccgccaagg tcatcatcga gcgctactac cccaagttga cgctcgactt tgagaccaac 180
 aagcgtcttt gcgatgagat cgctatcatt gcctccaagc gccttcgcaa caaggtgggc 240
 aatccatcac tgagccgtac aacagtcgga atttgacttg ctgacgaaaa ctagattgct 300
 ggttacacca cccaccttat gaagcgtatc cagcgtggcc ctgtccgcgg tatctctttc 360
 aagctgcagg aggaggagcg tgagcgcaag gatcagtacg ttcctgaggt ttccgctctg 420
 gatgtttccc agaccgagtc cggccagctc gatgtcgatg ccgacaccaa ggaccttctc 480
 aagtccatgg gcgtaagtcc tgttctcaac gcggttggtc gtggttttaa agcagtcctg 540
 taacttatat tgccactac agttcgacaa tctcaaggtc aacgttgtca acgtctcca 600
 acatcaggtt caggagcgcc cccgcgctt cggtag 637

<210> 29
 <211> 417
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 29
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 taccccaagt tgacgctcga ctttgagacc aacaagcgtc tttgcgatga gatcgctatc 120
 attgcctcca agcgcttctg caacaagatt gctggttaca ccaccacct tatgaagcgt 180
 atccagcgtg gccctgtccg cggatctctt ttcaagctgc aggaggagga gcgtgagcgc 240
 aaggatcagt acgttctctg gggttccgct ctggatgttt cccagaccga gtccggccag 300
 ctcgatgtcg atccgacac caaggacctt ctcaagtcca tgggcttcga caatctcaag 360
 gtcaacggtt tcaacgtctc ccaacatcag gttcaggagc gccccgcgcg cttccg 417

<210> 30
 <211> 139
 <212> PRT
 <213> *Aspergillus fumigatus*

<400> 30
 Met Gly Arg Val Arg Thr Lys Thr Val Lys Arg Ser Ala Lys Val Ile
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 Ile Glu Arg Tyr Tyr Pro Lys Leu Thr Leu Asp Phe Glu Thr Asn Lys
 20 25 30
 Arg Leu Cys Asp Glu Ile Ala Ile Ile Ala Ser Lys Arg Leu Arg Asn
 35 40 45
 Lys Ile Ala Gly Tyr Thr Thr His Leu Met Lys Arg Ile Gln Arg Gly
 50 55 60
 Pro Val Arg Gly Ile Ser Phe Lys Leu Gln Glu Glu Glu Arg Glu Arg
 65 70 75 80
 Lys Asp Gln Tyr Val Pro Glu Val Ser Ala Leu Asp Val Ser Gln Thr
 85 90 95
 Glu Ser Gly Gln Leu Asp Val Asp Ala Asp Thr Lys Asp Leu Leu Lys
 100 105 110

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Ser Met Gly Phe Asp Asn Leu Lys Val Asn Val Val Asn Val Ser Gln
 115 120 125

His Gln Val Gln Glu Arg Pro Arg Arg Phe Arg
 130 135

<210> 31
 <211> 1035
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 31
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 gcaagaaggg tgtaagaag aggaccgttg atcctttctc caggaaggac gaatactctg 180
 ttaaggtatg tcgacgtgga ctgtgtaagt cgaccgcagc taatctatat caggcgctt 240
 ccactttcca gatcagagag tatgttgac gcatatgat tCGaatgcag gataaaggcg 300
 attcacaatg gtagtggaga ttatgctgac tgaattatag tgtcgggaag actctggtca 360
 accgcaccag tgggtctcaag aacgccaatg actccctgaa gggtcgaatt ttcgagggtc 420
 cgctggctga cctgcagaat gatgaagacc atgctttccg caaggttaag cttcgtgtgg 480
 acgaggttca gggcaagaac tgtttgacca actccacgg tcttgatttc acaaccgaca 540
 aattgcgac cctcgtgcgc aagtggcagt cgctgatcga agccatgtca ctgtgaagac 600
 gaccgatgat tatctccttc ggctttttgc tatcgcttc accaagagac gcccgacca 660
 gattaagaag accacatatg ctggttcttc tcaaatccgt gccatccgca agaagatgat 720
 tgaaatcatg cagagggagg cagccagctg ctctctcgt cagctcactc acaagctcat 780
 tcttgaggtc attggtcgtg agatcgagaa ggctacccag ggaatctatc ctttgcaaaa 840
 tgtgtgtgac cctgttattc ttactcgga tgaagactaa ctgcaatcta ggtccatatt 900
 cgcaaggta agcttcttaa ggctcccaag ttcgacctgg gtgactgct gaatctgcac 960
 ggtgaatcta caaccgatga taagggccac aagggtcgaga gagagttcaa ggagcaggtt 1020
 ctcgaaagcg ttttaa 1035

<210> 32
 <211> 768
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 32
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 gttgatcctt tctccaggaa ggacgaatac tctgttaagg cgccttcac tttccagatc 120
 agagatgtcg ggaagactct ggtcaaccgc accagtggtc tcaagaacgc caatgactcc 180
 ctgaagggtc gaattttcga ggtctcgtg gctgacctgc agaagatga agaccatgct 240
 ttccgcaagg ttaagcttcg tgtggacgag gttcagggca agaactgttt gaccaacttc 300
 cacggtcttg atttcacaac cgacaaattg cgatccctcg tgcgcaagtg gcagtcgctg 360
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 gccttcacca agagacgccc gaaccagatt aagaagacca catatgctcg ttcttctcaa 480
 atccgtgcca tccgcaagaa gatgattgaa atcatgcaga gggaggcagc cagctgctct 540
 ctgctcagc tcaactcaca gctcattcct gaggtcattg gtcgtgagat cgagaaggct 600
 acccagggaa tctatccttt gcagaatgtc catattcgca aggtcaagct tcttaaggct 660
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 ggccacaagg tcgagagaga gttcaaggag caggttctcg aaagcgtt 768

<210> 33
 <211> 256
 <212> PRT
 <213> *Aspergillus fumigatus*

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PCT/IB03/01374

<400> 33

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Met Ala Val Gly Lys Asn Lys Arg Leu Ser Lys Gly Lys Lys Gly Val
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Lys Lys Arg Thr Val Asp Pro Phe Ser Arg Lys Asp Glu Tyr Ser Val
          20           25           30

Lys Ala Pro Ser Thr Phe Gln Ile Arg Asp Val Gly Lys Thr Leu Val
          35           40           45

Asn Arg Thr Ser Gly Leu Lys Asn Ala Asn Asp Ser Leu Lys Gly Arg
 50           55           60

Ile Phe Glu Val Ser Leu Ala Asp Leu Gln Asn Asp Glu Asp His Ala
 65           70           75           80

Phe Arg Lys Val Lys Leu Arg Val Asp Glu Val Gln Gly Lys Asn Cys
          85           90           95

Leu Thr Asn Phe His Gly Leu Asp Phe Thr Thr Asp Lys Leu Arg Ser
          100          105          110

Leu Val Arg Lys Trp Gln Ser Leu Ile Glu Ala Asn Val Thr Val Lys
          115          120          125

Thr Thr Asp Asp Tyr Leu Leu Arg Leu Phe Ala Ile Ala Phe Thr Lys
          130          135          140

Arg Arg Pro Asn Gln Ile Lys Lys Thr Thr Tyr Ala Arg Ser Ser Gln
          145          150          155          160

Ile Arg Ala Ile Arg Lys Lys Met Ile Glu Ile Met Gln Arg Glu Ala
          165          170          175

Ala Ser Cys Ser Leu Ala Gln Leu Thr His Lys Leu Ile Pro Glu Val
          180          185          190

Ile Gly Arg Glu Ile Glu Lys Ala Thr Gln Gly Ile Tyr Pro Leu Gln
          195          200          205

Asn Val His Ile Arg Lys Val Lys Leu Leu Lys Ala Pro Lys Phe Asp
          210          215          220

Leu Gly Ala Leu Leu Asn Leu His Gly Glu Ser Thr Thr Asp Asp Lys
          225          230          235          240

Gly His Lys Val Glu Arg Glu Phe Lys Glu Gln Val Leu Glu Ser Val
          245          250          255

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<210> 34

<211> 614

<212> DNA

<213> *Aspergillus fumigatus*

<400> 34

cctgtcggag atgatcaaag gcagcacctc gaattttcga ggaacactgc gaatagtttc 60

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aatcatgtat atggacccat tttcccgtca ccagaagcaa ttatatgtaa gtgggtttttg 120
cttctggcgg aacgggtcctg tgttgggaaa ttgacggcta tcaatagcgc ctgctaaacg 180
ggttatgtcc ctcaagaac cgacgttgaa aatgtccaag tcccatgccg acagacgctc 240
aaggatcatt cttacggatt cgccgcgaga aatctccaaa aagatcaatg ctgcgctcac 300
agactcggaa ttaaccatta catatgaccc agtccgtcga cctggagtgg cgaatttaat 360
agagatcttg agtcacttcg atggacgaac ttgcatgag attgccatgg aataccgttc 420
agccagtctt cgcgctctaa aggaacatct ggccagaacg ttgtccaatc atcttgagcc 480
aataagagag aagtatctct cactttagg agatcagact gactaccttg attctatagc 540
agaacagggt tctgaagccg cgcgggccaac cgctgaattg acaatggagc aagtcaaagt 600
cgctatgggc ttaa                                     614

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<210> 35

<211> 552

<212> DNA

<213> *Aspergillus fumigatus*

<400> 35

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gttatgtccc tcaagaacac gacgttgaaa atgtccaagt cccatgccga cagacgctca 180
aggatcattc ttacggattc gccgcgagaa atctccaaaa agatcaatgc tgcgctcaca 240
gactcggaat taaccattac atatgaccca gtccgtcgac ctggagtggc gaatttaata 300
gagatcttga gtcacttcga tggacgaact tgcgatgaga ttgccatgga ataccgttca 360
gccagtcttc gcgctctaaa ggaacatctg gccagaacgt tgtccaatca tottgagcca 420
ataagagaga agtatctctc actttagga gatcagactg actaccttga ttctatagca 480
gaacagggtt ctgaagccgc gcgggccaac gctgaattga caatggagca agtcaaagtc 540
gctatgggct ta                                     552

```

<210> 36

<211> 184

<212> PRT

<213> *Aspergillus fumigatus*

<400> 36

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Pro Val Gly Asp Asp Gln Arg Gln His Leu Glu Phe Ser Arg Asn Thr
  1              5              10              15

Ala Asn Ser Phe Asn His Val Tyr Gly Pro Ile Phe Pro Ser Pro Glu
      20              25              30

Ala Ile Ile Ser Pro Ala Lys Arg Val Met Ser Leu Lys Glu Pro Thr
      35              40              45

Leu Lys Met Ser Lys Ser His Ala Asp Arg Arg Ser Arg Ile Ile Leu
      50              55              60

Thr Asp Ser Pro Ala Glu Ile Ser Lys Lys Ile Asn Ala Ala Leu Thr
      65              70              75              80

Asp Ser Glu Leu Thr Ile Thr Tyr Asp Pro Val Arg Arg Pro Gly Val
      85              90              95

Ala Asn Leu Ile Glu Ile Leu Ser His Phe Asp Gly Arg Thr Cys Asp
      100             105             110

Glu Ile Ala Met Glu Tyr Arg Ser Ala Ser Leu Arg Ala Leu Lys Glu
      115             120             125

His Leu Ala Arg Thr Leu Ser Asn His Leu Glu Pro Ile Arg Glu Lys

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130

135

140

Tyr Leu Ser Leu Val Gly Asp Gln Thr Asp Tyr Leu Asp Ser Ile Ala
 145 150 155 160

Glu Gln Gly Ser Glu Ala Ala Arg Ala Asn Ala Glu Leu Thr Met Glu
 165 170 175

Gln Val Lys Val Ala Met Gly Leu
 180

<210> 37

<211> 819

<212> DNA

<213> *Aspergillus fumigatus*

<400> 37

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atggcaactt cgactgggac cggatgggct cagctccggc agcaagcccg ttcgcttgag 60
actcaggtac ggaactcgaa actacgctat aatgaggctt tactcgtgat ttggatgttg 120
acaataatgt tcctagaccg agagtctgtt tcacacctat gcgcagtatg catcgatgac 180
gaagctgcct ccgaaaccct cagaagaaga acaacggatt gaatcgcaac tgaaggatct 240
tcttgaaaag gtgtgcactt tgaggccctc tagtccagcc caacagacga tcatgctgac 300
acgatccgat catagcgtga agccctcctc tcccagctct cccgtctcct tgactccgaa 360
gccactctta ccgcatctgc cctgaaacag agcaatcttg cccgcaatcg cgaagtcctc 420
caggatcatc gccgcgaatt gcagcgcctg aacgcgcgaa tcgccgagtc ccgcgaccga 480
gccaatcttc tgtctaactg ccgctccgac attgatgcct accgcaattc aaaccccgcc 540
gcggtgagg cagactacat gctcgaggag cggggtcgta tagatgaaag ccataacatg 600
atagatggtg tcctaagcca ggcgtatgca atcaacgaga gttttgggct acaacgtgaa 660
accctggcca gcatcaatcg ccgtatcgtc ggtgctgcca ataaggtaac aggaatgaat 720
gcattgattg gtaagattgg gacgaagagg agacgtgacg caatcatctt gggggctttc 780
atcggtcttt gtttcttgat ggtgttcttc ttccgatga 819

```

<210> 38

<211> 681

<212> DNA

<213> *Aspergillus fumigatus*

<400> 38

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<210> 39

<211> 227

<212> PRT

<213> *Aspergillus fumigatus*

<400> 39

WO 03/076464

PCT/IB03/01374

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Arg Ser Leu Glu Thr Gln Thr Glu Ser Leu Phe His Thr Tyr Ala Gln
 20 25 30

Tyr Ala Ser Met Thr Lys Leu Pro Pro Lys Pro Ser Glu Glu Glu Gln
 35 40 45

Arg Ile Glu Ser Gln Leu Lys Asp Leu Leu Glu Lys Arg Glu Ala Leu
 50 55 60

Ile Ser Gln Leu Ser Arg Leu Leu Asp Ser Glu Ala Thr Leu Thr Ala
 65 70 75 80

Ser Ala Leu Lys Gln Ser Asn Leu Ala Arg Asn Arg Glu Val Leu Gln
 85 90 95

Asp His Arg Arg Glu Leu Gln Arg Leu Asn Ala Ala Ile Ala Glu Ser
 100 105 110

Arg Asp Arg Ala Asn Leu Leu Ser Asn Val Arg Ser Asp Ile Asp Ala
 115 120 125

Tyr Arg Asn Ser Asn Pro Ala Ala Ala Glu Ala Asp Tyr Met Leu Glu
 130 135 140

Glu Arg Gly Arg Ile Asp Glu Ser His Asn Met Ile Asp Gly Val Leu
 145 150 155 160

Ser Gln Ala Tyr Ala Ile Asn Glu Ser Phe Gly Leu Gln Arg Glu Thr
 165 170 175

Leu Ala Ser Ile Asn Arg Arg Ile Val Gly Ala Ala Asn Lys Val Pro
 180 185 190

Gly Met Asn Ala Leu Ile Gly Lys Ile Gly Thr Lys Arg Arg Arg Asp
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Phe Phe Arg
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<210> 40

<211> 1601

<212> DNA

<213> *Aspergillus fumigatus*

<400> 40

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WO 03/076464

PCT/IB03/01374

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<210> 41

<211> 1182

<212> DNA

<213> *Aspergillus fumigatus*

<400> 41

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<210> 42

<211> 394

<212> PRT

<213> *Aspergillus fumigatus*

<400> 42

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20           25           30

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PCT/IB03/01374

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 65 70 75 80
 Arg Ile Val Arg His Pro Asn Ile Val Glu Leu Lys Ala Phe Tyr Tyr
 85 90 95
 Ser Asn Gly Glu Arg Lys Asp Glu Val Tyr Leu Asn Leu Val Leu Glu
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 Tyr Val Pro Glu Thr Val Tyr Arg Ala Ser Arg Tyr Phe Asn Lys Leu
 115 120 125
 Lys Thr Thr Met Pro Met Leu Glu Val Lys Leu Tyr Ile Tyr Gln Leu
 130 135 140
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 145 150 155 160
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 Leu Cys Asp Phe Gly Ser Ala Lys Ile Leu Val Glu Asn Glu Pro Asn
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 Val Ser Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala Pro Glu Leu Ile Phe
 195 200 205
 Gly Ala Thr Asn Tyr Thr Thr Lys Ile Asp Val Trp Ser Thr Gly Cys
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 Val Met Ala Glu Leu Met Leu Gly Gln Pro Leu Phe Pro Gly Glu Ser
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 Gly Ile Asp Gln Leu Val Glu Ile Ile Lys Val Leu Gly Thr Pro Thr
 245 250 255
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 260 265 270
 Pro Gln Ile Lys Pro His Pro Phe Asn Lys Val Phe Arg Arg Ala Pro
 275 280 285
 His Glu Ala Ile Asp Leu Ile Ser Ala Leu Leu Glu Tyr Thr Pro Thr
 290 295 300
 Gln Arg Leu Ser Ala Ile Glu Ala Met Cys His Pro Phe Phe Asp Glu
 305 310 315 320
 Leu Arg Asp Pro Asn Thr Arg Leu Pro Asp Ser Arg His Pro Gly Gly
 325 330 335
 Ala Ala Arg Asp Leu Pro Asn Leu Phe Asp Phe Ser Arg His Glu Leu
 340 345 350
 Ser Ile Ala Pro Ala Leu Asn Ser Arg Leu Val Pro Pro His Ala Arg

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PCT/IB03/01374

355 360 365
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Thr Lys Glu Glu Met Met Ala Arg Leu Asp
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<210> 43
<211> 2209
<212> DNA
<213> *Aspergillus fumigatus*

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<210> 44
<211> 2209
<212> DNA
<213> *Aspergillus fumigatus*

<400> 44

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<210> 45

<211> 735

<212> PRT

<213> *Aspergillus fumigatus*

<400> 45

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 20 25 30

Gln His Gly Asn Trp Leu Tyr Leu Phe Glu Ser Val Thr Ser Gly Cys
 35 40 45

Phe Ile Lys Ser Met Trp Lys Ser Phe Lys Glu Lys His Ala Ser Lys
 50 55 60

Phe Gly Gly Gly Ser Ala Glu Ala Ala Ala Ser Asp Gly Gly Gln Asp
 65 70 75 80

Leu Thr Thr Ile Leu Asp Arg Ser Gln Arg Gly Glu Leu Thr Val Leu

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Glu Ala Ala His Gln Asp His Arg Leu Arg Val Thr Ile Gly Val Thr
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 Gly Trp Leu Thr Glu Glu Asp Asn Phe Val Ile Pro Trp Arg Val Ile
 435 440 445
 Gly Ala Glu Ser Glu Val Phe Gly Leu Arg Trp Glu Thr Glu Pro Leu
 450 455 460
 Met Asn Leu Gly Asn Ala Leu Asp Leu Leu Val Thr Ser Ala Ala Trp
 465 470 475 480
 Thr Ala Gly Glu Gln Val Leu Lys Lys Thr Phe Leu Ser Gln Leu Leu
 485 490 495
 Thr Ala Val Ala Leu Pro Leu Gly Leu Leu Lys Val Ala Arg Val Val
 500 505 510
 Asp Asn Pro Phe Ser Val Ala Lys Ala Arg Ala Asp Lys Ala Gly Glu
 515 520 525
 Val Leu Ala Asp Ala Leu Ile Ser Lys Val Gln Gly Glu Arg Pro Val
 530 535 540
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 545 550 555 560
 Gln Ser Leu Ala Lys Arg Arg Ala Phe Gly Leu Val Glu Ser Ala Ile
 565 570 575
 Leu Met Gly Ala Pro Thr Pro Ser Asn Ser Glu Gln Trp Cys Arg Ile
 580 585 590
 Arg Ser Val Val Ser Gly Arg Leu Val Asn Val Tyr Ser Glu Asn Asp
 595 600 605
 Ser Val Leu Ala Leu Leu Tyr Arg Thr Ser Ser Leu Gln Leu Gly Val
 610 615 620
 Ala Gly Leu Gln Pro Val Glu Gly Val Ser Gly Val Glu Asn Leu Asp
 625 630 635 640
 Val Ser Asp Leu Ile Ser Gly His Leu Arg Tyr Gln Phe Leu Val Gly
 645 650 655
 Arg Ile Leu Ser Val Val Gly Leu Glu Ser Ile Asp Ala Arg Glu Val
 660 665 670
 Ala Leu Glu Glu Ala Ala Leu Glu Ala Lys Asp Arg Arg Gln Glu Gln
 675 680 685
 Glu Arg Ala His Asn Glu Arg Gln Ala Gly Phe Met Gly Glu Gly Arg
 690 695 700
 Ser Pro Ser Gln Arg Leu Glu Ser Gln Glu Asp Leu Gln Gly Glu Glu
 705 710 715 720
 Asp Arg Leu Gln Lys Glu Met Gly Lys Ala Arg Val Arg His Ser
 725 730 735

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PCT/IB03/01374

<210> 46
 <211> 510
 <212> DNA
 <213> *Aspergillus fumigatus*

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<210> 47
 <211> 423
 <212> DNA
 <213> *Aspergillus fumigatus*

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<210> 48
 <211> 141
 <212> PRT
 <213> *Aspergillus fumigatus*

<400> 48
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 20 25 30
 Ala Ile Val Glu Ile Ile Asp His Lys Arg Val Leu Val Asp Gly Pro
 35 40 45
 Ser Thr Glu Glu Asn Lys Ile Val Pro Arg His Ala Leu Pro Leu Ala
 50 55 60
 His Ala Thr Leu Thr Pro Phe Val Ile Pro Lys Leu Pro Arg Ala Ala
 65 70 75 80
 Gly Thr Gly Pro Val Lys Lys Leu Trp Glu Lys Asn Glu Ile Asp Gly
 85 90 95
 Lys Trp Ala Lys Ser Thr Ile Ala Gln Lys Thr Glu Arg Ala Glu Arg
 100 105 110

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PCT/IB03/01374

Arg Lys Asn Leu Thr Asp Phe Glu Arg Phe Lys Val Leu Arg Leu Lys
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Lys Gln Val Arg Ser Val Cys Glu Thr Met Gly Glu Leu
 130 135 140

<210> 49

<211> 1413

<212> DNA

<213> *Aspergillus fumigatus*

<400> 49

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```

<210> 50

<211> 1284

<212> DNA

<213> *Aspergillus fumigatus*

<400> 50

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gcaacagcag ttccccgggt cactcaaaat gcggctgggt ccaaaggccc cacggcaatg 180
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atcgctaagc gcagaacccc aaagatccaa cggcaatact cggatatttg tggaggggtca 360
ccgatcagga aatgggtccga gtatcagtg caggaaatgt gcagattgct agacaaaatc 420
aatcccga aa cggctcctca caagccttac gtcgcgttcc ggtacgccga ccctctgacg 480
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ggtgccatcc agtggagtg cattgatcga tggccaacgc accctggcct cgtggaggct 720
ttcgccgga acattgagga gcagctgaag acataccag aggagaagcg aaacggtgtc 780
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cctgctgaag ttgctgcaac tgtgcatgct gtcattgcaaa gattgaattt cagcaatcct 900
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gatacggctg aaaactatgt caaacgtgga cagaccgata ttattctagt tcccattgcc 1020
ttcaccagcg accatattga gactctgtac gagttggatc tggaagtgat aaaggaagca 1080
aactccccgg gagtcaagag agccgagagt ttgaatggta accccatttt cattcaggca 1140
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```

<210> 51

<211> 428

<212> PRT

<213> *Aspergillus fumigatus*

<400> 51

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Met Ala Leu Arg Arg Pro Leu Thr Leu Pro Arg His Ile Leu Asn Gly
  1             5             10             15

Ala Cys Leu Gly Leu Arg Pro Ala Val Ser Arg Ala Ala Leu Ala Tyr
      20             25             30

Gly Gln Glu Gln Arg Lys Gly Leu Ala Thr Ala Val Pro Pro Val Thr
      35             40             45

Gln Asn Ala Ala Gly Ser Lys Gly Pro Thr Ala Met Val Phe Leu Asn
      50             55             60

Met Gly Gly Pro Ser Lys Ile Asp Glu Val Glu Asp Phe Leu Ser Arg
      65             70             75             80

Leu Phe Ala Asp Gly Asp Leu Ile Pro Leu Gly Arg Leu Gln Ser Tyr
      85             90             95

Leu Gly Pro Leu Ile Ala Lys Arg Arg Thr Pro Lys Ile Gln Arg Gln
      100            105            110

Tyr Ser Asp Ile Gly Gly Gly Ser Pro Ile Arg Lys Trp Ser Glu Tyr
      115            120            125

Gln Cys Glu Glu Met Cys Arg Leu Leu Asp Lys Ile Asn Pro Glu Thr
      130            135            140

Ala Pro His Lys Pro Tyr Val Ala Phe Arg Tyr Ala Asp Pro Leu Thr
      145            150            155            160

Glu Glu Met Tyr Thr Lys Leu Leu Glu Asp Gly Phe Gly Asn Gly Lys
      165            170            175

Gly Gly Arg Ala Val Ala Phe Thr Gln Tyr Pro Gln Tyr Ser Cys Ser
      180            185            190

Thr Thr Gly Ser Ser Leu Asn Glu Leu Trp Lys Trp Arg Thr Arg Leu
      195            200            205

Glu Gly Lys Arg Ala Asn Gly Asn Met Asp Pro Ala Gly Ala Ile Gln
      210            215            220

Trp Ser Val Ile Asp Arg Trp Pro Thr His Pro Gly Leu Val Glu Ala
      225            230            235            240

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Phe Ala Arg Asn Ile Glu Glu Gln Leu Lys Thr Tyr Pro Glu Glu Lys
 245 250 255
 Arg Asn Gly Val Val Leu Leu Phe Ser Ala His Ser Leu Pro Met Ser
 260 265 270
 Val Val Asn Arg Gly Asp Pro Tyr Pro Ala Glu Val Ala Ala Thr Val
 275 280 285
 His Ala Val Met Gln Arg Leu Asn Phe Ser Asn Pro Tyr Arg Leu Cys
 290 295 300
 Trp Gln Ser Gln Val Gly Pro Ser Ala Trp Leu Gly Ala Gln Thr Ser
 305 310 315 320
 Asp Thr Val Glu Asn Tyr Val Lys Arg Gly Gln Thr Asp Ile Ile Leu
 325 330 335
 Val Pro Ile Ala Phe Thr Ser Asp His Ile Glu Thr Leu Tyr Glu Leu
 340 345 350
 Asp Leu Glu Val Ile Lys Glu Ala Asn Ser Pro Gly Val Lys Arg Ala
 355 360 365
 Glu Ser Leu Asn Gly Asn Pro Ile Phe Ile Gln Ala Leu Ala Asp Ile
 370 375 380
 Ala Gln Glu His Leu Arg Lys Gly Glu Lys Cys Ser Leu Gln Met Thr
 385 390 395 400
 Leu Arg Cys Gln Gly Cys Lys Ser Glu Arg Cys Leu Glu Gln Lys Lys
 405 410 415
 Phe Phe Ala Gly Asp Arg Phe Ser Ser Leu Val Val
 420 425

<210> 52

<211> 1536

<212> DNA

<213> *Aspergillus fumigatus*

<400> 52

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 ttctcctcat ctcggtgctg ggctggcatt gccgatcatg aatcaactcc ctgcactgtc 180
 caaaagacct atttttctgc caatcggacc gcagatggct tacttgcate cttatccgcc 240
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 gcgctctccg ccagtaatat ctgtctctat gcctttgtgt atacgccgct gaagcgtata 900
 tcagtgatca acacctgggt aggcgcctg gtaggaggca ttctccggt gatgggttg 960
 accgctgcag caggccagac agcgaccact ggccacgaca gctggcgagg catgttggtc 1020

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```

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ctcgcattga ctaatcccgc cgcaaatgcc cgtgtcgcac tacgatattc tcttctcatg 1200
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gccaacggca gtgtctcgac cctcttcttg gccagtattt ggcagctgcc aatcctcctt 1380
gtcgggtggtc tggtcacgaa gaaaggtctc tgggatggtg tctggaacaa tgttttcgg 1440
cagcctgttg aagacgagga tgactatctc tgggaggatg aggatgaagt ggcagaggcg 1500
gagcgcaaga tgatacctgc gaagacgagt agctcgc 1536

```

<210> 53

<211> 1536

<212> DNA

<213> *Aspergillus fumigatus*

<400> 53

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ttctcctcat ctcggctgcg ggctggcatt gccgatcatg aatcaactcc ctcgactgtc 180
caaaagacct atttttctgc caatcggacc gcagatggct tacttgcatc cttatccgcc 240
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gagtcgatta cttcacagtc tacttcacaa gaggtaacct atcgccggag gaagcggtta 360
aaggaagagg cggccaagaa taatgctgca gaaaccgaac tccctcctga tgccctgctc 420
caattgtcca cctctctatc agccctccct gcgacttccc tgcgccgcaa gctggctgcg 480
tttctcgccc tcacaaagcc tegtctctcg ttctctgatc tgttgacgac tacctccgct 540
tatgggatgt acccgatctc ctctcttctc acacttgacc cttcaatgac tcccctaccg 600
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```

<210> 54

<211> 512

<212> PRT

<213> *Aspergillus fumigatus*

<400> 54

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Met Ile Tyr Leu Arg Ser Ser Leu Leu Arg Ser Gly Leu Ala Arg Asp
  1                               5                               10                               15

```

```

Pro Ala Arg Leu Cys Ser Gln Cys Phe Ser Arg Leu Ser Pro Ser Arg
      20                               25                               30

```

```

Arg Pro Val Ala Val Arg Ser Phe Phe Ser Ser Ser Arg Leu Arg Ala
      35                               40                               45

```

```

Gly Ile Ala Asp His Glu Ser Thr Pro Ser Thr Val Gln Lys Thr Tyr

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50	55	60
Phe Ser Ala Asn Arg Thr 65	Ala Asp Gly Leu Leu 70	Ala Ser Leu Ser Ala 75
Val Asn Ser Ser Pro Arg Ser Ile Ala Asp Asn Ala Leu Ser Gln Gly 85		95
Ala Ala Ser Ser Glu Ser Ile Thr Ser Gln Ser Thr Ser Gln Glu Leu 100	105	110
Pro His Arg Arg Arg Lys Arg Leu Lys Glu Glu Ala Ala Lys Asn Asn 115	120	125
Ala Ala Glu Thr Glu Leu Pro Pro Asp Ala Ser Ser Gln Leu Ser Thr 130	135	140
Leu Ser Ser Ala Leu Pro Ala Thr Ser Leu Arg Arg Lys Leu Ala Ala 145	150	155
Phe Leu Ala Leu Thr Lys Pro Arg Leu Ser Phe Leu Ile Val Leu Thr 165	170	175
Thr Thr Ser Ala Tyr Gly Met Tyr Pro Ile Ser Ser Leu Leu Thr Leu 180	185	190
Asp Pro Ser Met Thr Pro Leu Pro Thr Leu Ser Thr Ser Thr Leu Thr 195	200	205
Phe Leu Tyr Leu Thr Thr Gly Thr Phe Leu Ser Ser Cys Ser Ala Asn 210	215	220
Thr Leu Asn Met Leu Leu Glu Pro Lys Tyr Asp Ala Leu Met Ser Arg 225	230	235
Thr Arg Asn Arg Pro Leu Val Arg Gly Leu Leu Ser Arg Arg Ala Ala 245	250	255
Val Leu Phe Ala Ile Ala Thr Ala Ala Gly Leu Gly Leu Leu Tyr 260	265	270
Ile Gly Thr Asn Pro Thr Thr Thr Ala Leu Ser Ala Ser Asn Ile Cys 275	280	285
Leu Tyr Ala Phe Val Tyr Thr Pro Leu Lys Arg Ile Ser Val Ile Asn 290	295	300
Thr Trp Val Gly Ala Val Val Gly Gly Ile Pro Pro Leu Met Gly Trp 305	310	315
Thr Ala Ala Ala Gly Gln Thr Ala Thr Thr Gly His Asp Ser Trp Arg 325	330	335
Asp Met Leu Phe Ser Lys Asp Ser Ile Gly Gly Trp Leu Leu Gly Gly 340	345	350
Ile Leu Phe Ala Trp Gln Phe Pro His Phe Asn Ala Leu Ser Tyr Met 355	360	365
Ile Arg Glu Glu Tyr Lys Ala Ala Gly Tyr Arg Met Leu Ala Trp Thr 370	375	380

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Asn Pro Ala Ala Asn Ala Arg Val Ala Leu Arg Tyr Ser Leu Leu Met
385                      390                      395                      400

Phe Pro Phe Ser Val Gly Leu Trp Trp Val Gly Val Val Gly Asn Gly
                      405                      410                      415

Phe Leu Val Gly Ser Thr Ala Ala Asn Gly Trp Leu Val Lys Glu Ala
                      420                      425                      430

Tyr Lys Phe Trp Arg His Gln Gly Ala Asn Gly Ser Ala Arg Arg Leu
                      435                      440                      445

Phe Trp Ala Ser Ile Trp Gln Leu Pro Ile Leu Leu Val Gly Gly Leu
                      450                      455                      460

Val Thr Lys Lys Gly Leu Trp Asp Gly Val Trp Asn Asn Val Phe Gly
465                      470                      475                      480

Gln Pro Val Glu Asp Glu Asp Asp Tyr Leu Trp Glu Asp Glu Asp Glu
                      485                      490                      495

Val Ala Glu Ala Glu Arg Lys Met Ile Pro Ala Lys Thr Ser Ser Ser
                      500                      505                      510

```

<210> 55
 <211> 1626
 <212> DNA
 <213> *Aspergillus fumigatus*

```

<400> 55
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PCT/IB03/01374

```

gcaagtctca agcgctggga tgacagtga cgggccgcga acgttagtat cctgacacgg 1560
gccctgcaag caaacttttc tgattttgaa aatctacgcg ccaaatacgt taagctcaac 1620
gcgacc                                     1626

```

<210> 56

<211> 1626

<212> DNA

<213> *Aspergillus fumigatus*

<400> 56

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atgctcaacg ccgcggttgc tgccccgcga tgttttgtat atccccactga tcgcgcagca 60
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ttccgtcgac agttgcatgc ttccggcgtc cgatcaattg aacctgttat ctttcgaaat 180
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gctggtcacg atcaatcatc tcaaaaggcc tcctccgtgt caaatgcaga gtcagagtcc 360
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gatgccgttt cgcgtctcga cgcggagatc cgcgctcttg agctctacat gacaccgacc 600
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gcgacc                                     1626

```

<210> 57

<211> 542

<212> PRT

<213> *Aspergillus fumigatus*

<400> 57

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Met Leu Asn Ala Ala Val Ala Ala Pro Arg Cys Phe Val Tyr Pro Thr
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Asp Arg Ala Ala Met Arg Leu Gly Phe Ala Leu Arg Leu Ser Ser Pro
      20                      25                      30

Ala Pro Leu Phe Ser Thr Ala Pro Phe Arg Arg Gln Leu His Ala Ser
      35                      40                      45

Gly Val Arg Ser Ile Glu Pro Val Ile Phe Arg Asn Ser Leu Glu Lys
      50                      55                      60

Thr Leu Glu Ala His Arg Ser Ser Asn Arg Ala Ser Leu Ile Arg Lys
      65                      70                      75                      80

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Val Ile Asn His Asp Cys Pro Ala Glu Thr Pro Pro Pro Ile Leu Pro
 85 90 95
 Leu Glu Asn Arg Ala Gly His Asp Gln Ser Ser Gln Lys Ala Ser Ser
 100 105 110
 Val Ser Asn Ala Glu Ser Glu Ser Pro Arg Ser Ser Ala Pro Ala Arg
 115 120 125
 Arg Ala Gln Arg Lys Ala Arg Ser Pro Ser Gln Val Ala Thr Pro Gln
 130 135 140
 Pro Gln Thr Thr Glu Tyr Pro Gln Leu Gln Trp His Ala Asp Glu Thr
 145 150 155 160
 Lys Gly Arg Pro Ala Gln Ser Pro Trp Leu Lys Tyr Leu Thr Thr Asp
 165 170 175
 Trp Lys Thr Pro Asp Ala Val Ser Arg Leu Asp Ala Glu Ile Arg Ala
 180 185 190
 Leu Glu Leu Tyr Met Thr Pro Thr Pro Ser Glu Arg Thr Glu Ile Asp
 195 200 205
 Arg Leu Val Ala Asp Met Gly Arg Leu Leu Ala Gly Ile Val Pro Ser
 210 215 220
 Pro Pro Gln Val Thr Gly Ser Trp Arg Thr Arg Phe Ala Leu Ser His
 225 230 235 240
 Ser Gly Leu Asp Phe Val Leu Pro Val Pro Asp Ser Asp Arg Ser Thr
 245 250 255
 Arg Asp Val Arg Lys Pro Ser Ala Thr Arg Pro Lys Val Leu Gln Thr
 260 265 270
 Tyr Lys Lys Leu Leu His Glu Val Gly His Ala Leu Gln Gln Ser Pro
 275 280 285
 Ser Phe Ala Glu Arg Val Arg Ile Ile Gly Ser Arg Phe Pro Val Leu
 290 295 300
 Ser Ala Ile His Arg Pro Thr Gly Arg Leu Leu Gln Phe His Cys Gly
 305 310 315 320
 Glu Gly Leu Pro Ala Ser Val Glu Tyr Ile Met Asp Tyr Gln Ala Glu
 325 330 335
 Tyr Pro Ser Ile Arg Pro Leu Tyr Val Thr Ala Arg Leu Ile Leu Glu
 340 345 350
 Ala Arg Gly Arg Tyr Gly Arg Thr Gln Met Ser Ile Glu Ser Asp Ala
 355 360 365
 Leu Val Met Leu Leu Val Ala Phe Leu Lys Met Asn His Gly Arg Phe
 370 375 380
 Gln Arg Pro Asp Cys Leu Gly Glu Gln Leu Ile Ala Phe Leu Arg Ala
 385 390 395 400

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PCT/IB03/01374

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 420 425 430
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 435 440 445
 Ser Leu Lys Arg Thr Ala Ala Ala Arg Arg Asn Leu Pro Ala Ala Ser
 450 455 460
 Arg Leu Cys Val Gln Asp Pro Thr Asn Tyr Met Asn Asp Leu Gly Arg
 465 470 475 480
 Ser Cys Val Arg Thr Leu Glu Leu Gln His Thr Phe Ser Leu Ala His
 485 490 495
 Asp Arg Leu Gly Ala Ser Leu Lys Arg Trp Asp Asp Ser Glu Pro Ala
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<212> DNA

<213> *Aspergillus fumigatus*

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PCT/IB03/01374

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<212> PRT

<213> *Aspergillus fumigatus*

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Leu	Glu	Ser	Ely	Leu	Gly	Arg	Arg	Asn	Phe	Val	Pro	Pro	Arg	Gln	Val
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Pro	Val	Val	Asp	Ala	Met	Glu	Arg	Thr	Lys	Asn	Ala	Ile	Gln	Ser	Asn
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Asn	Ser	Ser	Asr	Arg	Ala	Gln	Leu	Ser	Asp	Ala	Leu	Pro	Glu	Ser	Glu
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Lys	Ser	Gln	Asr	Ala	Gly	Gln	Val	Ile	Val	Pro	Thr	Arg	Met	Gln	Glu
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Leu	Leu	Asp	Arg	Gly	Arg	Pro	Ile	Glu	Ala	Ala	Gln	Phe	Phe	Leu	Glu
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Thr	His	Ala	Ala	Ser	Leu	Lys	Gly	Ile	Ser	Ser	Asp	Arg	Lys	Glu	Met
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Ala	Thr	Lys	Val	Phe	Phe	Val	Asn	Cys	Lys	Glu	Asp	Asn	Val	Phe	Ile
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Ala	Arg	Ser	Val	Phe	Glu	Arg	Leu	Glu	Glu	Val	Asp	Arg	Ile	Thr	Pro
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Glu	Met	Trp	Lys	Thr	Leu	Met	Leu	Ala	Leu	Ala	Lys	Lys	Gly	Cys	Ile
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Glu	Ser	Val	Ala	Ser	Val	Tyr	Thr	Arg	Tyr	Met	Arg	Lys	Phe	Pro	Cys
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Pro	Pro	Glu	Met	Val	Asp	Val	Val	Leu	Arg	Ser	Leu	Leu	Glu	Ser	His
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Arg	Asp	Cys	Ely	Leu	Cys	Gly	Ala	Tyr	Leu	Ser	Gly	Leu	Trp	Arg	Lys
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Val	Ile	Lys	Ala	Tyr	Val	Glu	Phe	Gly	Arg	Val	Ala	Asp	Ala	Glu	Ala
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Gly Val Asp Ala Gly Leu Gln Glu Met His Lys Leu Lys Leu Thr Arg 325		335
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Trp Val Ser His Ser Gly Ile Glu Ile Arg Asn Phe Val Phe Arg Tyr 355	360	365
Leu Asp Lys Phe Asp Ile Val Pro Asp Arg Val Leu Tyr Lys His Ile 370	375	380
Leu Glu Ala Phe Val Glu Lys Gly Asp Lys Glu Met Ile Ala Glu Phe 385	390	395
Thr Ser Met Ala Lys Gln Arg Ser Trp Asn Ile Pro Ile Asn Glu Gln 405	410	415
Gln Phe Leu Glu Ile Leu Arg Ser Arg Arg Leu Ala Leu Glu Gly Ala 420	425	430
Pro Val Gly Phe Trp Gln Met Leu Gln Ala Ala Arg Val Lys Tyr Gly 435	440	445
His Ser Ser Thr Ser Gln Arg Ile Met Gly Tyr Asp Gln Gln Ser Phe 450	455	460
Pro Leu Pro Glu Val Asn Ser Met Pro Tyr Thr Gln Asn Pro Leu Ser 465	470	475
Trp Tyr Gln Arg Thr Met Gln Glu Thr Thr Pro Ser Lys Pro Val Asp 485	490	495
Gln Tyr Gln Lys Leu His Lys Gln Met Thr His Phe Leu His Ala Gly 500	505	510
Lys Leu Lys Glu Ala Leu Lys Cys Phe Gln Asn Ala Lys Asn Ala Arg 515	520	525
Phe Gln Met Arg Gln Leu His Val Glu Leu Ala Val Ile Ala Thr Leu 530	535	540
Leu Glu Asp Gly Leu Ser Ala Ala Arg Ser Leu Ile Glu Ser Glu Trp 545	550	555
Arg Thr Ile Arg His Leu Val Arg Phe Ser Pro Ile Phe Phe Arg Gln 565	570	575
Val Met Ala Val Asp Glu Asp Ala Gly Gly His Ile Val Gln Met Ala 580	585	590
Val Leu Arg Phe Tyr Gln Leu Cys Trp Ser Thr Lys His Met Lys Val 595	600	605

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Lys His His Leu Thr Val Ala Thr Ser Arg Arg Leu Ile Ser Gln His
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Lys Pro Glu Met Ala Leu Glu Leu Leu Thr Ala Val Tyr Lys Ser Arg
625 630 635 640

Tyr Arg Phe Ala Ala Thr Phe Asp Gly Val Cys Met Lys Met Phe Ala
645 650 655

Arg Ala Phe Ala Ala Thr Asp Asn Ile Leu Gly Leu Arg Trp Cys Ile
660 665 670

Leu Thr Ala Leu Ser Arg Asp Ser Ala Leu Asn His Asp Phe Val Val
675 680 685

Glu Val Arg Arg Ile Leu Gly Thr Leu Ser Pro Pro Ser Ala Val Asp
690 695 700

Ala Thr Ala Gly Pro Val Thr His Glu Gln Leu Glu Tyr Leu Tyr Tyr
705 710 715 720

Ile Ala Asp Leu Leu Glu Glu Lys Asn Glu Gly Cys Ala Pro Ile Trp
725 730 735

Glu Leu Lys His Asp Ala Thr Leu Lys Gln Ser Ser Arg Arg Gln Leu
740 745 750

Lys Gln Pro Leu Asp Ala Ser Arg Leu Phe Asn Gln Ser Asp Val Arg
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Glu Thr Val Lys Arg Trp Asp Glu Glu Tyr Glu Leu Glu Ala Val Leu
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785

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21

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19

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<210> 70
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PCT/IB03/01374

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PCT/IB03/01374

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PCT/IB03/01374

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PCT/IB03/01374

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<223> PCR primer Gt11f1

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<210> 89

<211> 19

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<210> 91

<211> 3052

<212> DNA

<213> Aspergillus fumigatus

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PCT/IB03/01374

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<223> Phylum CEA228; clone 8-47; contig 4842 region 234347-231296
Genomic sequence containing 3' and 5'-ends and the coding region

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<210> 92

<211> 2052

WO 03/076464

PCT/IB03/01374

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA228; clone 8-47; contig 4842 region 234347-231296
Genomic sequence containing the coding region

<400> 92

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<210> 93

<211> 2052

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA228; clone 8-47; contig 4842 region 234347-231296
Coding region without introns

<400> 93

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PCT/IB03/01374

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<210> 94

<211> 683

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA228; clone 8-47; contig 4842 region 234347-231296
Protein sequence

<400> 94

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Ala Gln Arg Met Arg Asp Gly Ile Glu Gln Asn Phe Ser Asn Ala Pro
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Pro Ser Ser Gly Gln Ser Val Asn Tyr Glu Glu Lys Arg Thr Gly Ser
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Leu Pro Gln Ser Thr Asp Ala Gln Glu Asp Gln Ser Ser Ser Gly Ser
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 Ala Leu Ile Ser Lys Val Gln Gly Glu Arg Pro Val Thr Leu Ile Gly
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 Tyr Ser Leu Gly Ser Arg Val Ile Phe Ala Cys Leu Gln Ser Leu Ala
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 Lys Arg Arg Ala Phe Gly Leu Val Glu Ser Ala Ile Leu Met Gly Ala
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<210> 95

<211> 3814

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA229; clone 8-62; contig 4938 region 215653-219466
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 95

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PCT/IB03/01374

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PCT/IB03/01374

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<210> 96
 <211> 2814
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA229; clone 8-62; contig 4938 region 215653-219466
 Genomic sequence containing the coding region

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WO 03/076464

PCT/IB03/01374

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<213> *Aspergillus fumigatus*

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<223> Phylum CEA229; clone 8-62; contig 4938 region 215653-219466

Coding region without introns

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WO 03/076464

PCT/IB03/01374

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<213> *Aspergillus fumigatus*

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<223> Phylum CEA229; clone 8-62; contig 4938 region 215653-219466
Protein sequence

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PCT/IB03/01374

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PCT/IB03/01374

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<213> *Aspergillus fumigatus*

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WO 03/076464

PCT/IB03/01374

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Genomic sequence containing the coding region

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<210> 101

<211> 1200

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA230; clone 9-11; contig 4899 region 9642-7242
Coding region without introns

<400> 101

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tcagagac	cgaaatcat	ttcagctgc	aatcagacca	tattctctgg	gatccagcca	180
accggcgt	cgcaccttg	aaattatct	ggagctctac	gtgaatgggt	acggctacaa	240
aatgctgc	aggagggaa	aagattgtt	ttttctatc	tcgacttgca	tcggttgaca	300
gtgccaca	acgcctcca	gctacgaa	tggagaaa	agacatttgc	aacactcatt	360
gccgttgg	tagaccgaa	tcgctcaac	attttctacc	agtccgccgt	ccatgcacac	420
gccgaact	tttgatttt	gtgcacaata	gcctctatg	gatatctctc	ccgaatgaca	480
cagtggaa	aggaacagc	agctgacgc	ggccagagca	aactccagtt	gcctgataac	540
gcaaactcg	aagactcgac	ggcgaggtca	aggttgcat	tgggttgg	ctcataccct	600
gttctgcagg	cggcggatat	tctaatacaga	gctactcatg	ttcctgtcgg	agatgatcaa	660
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ccgacgttg	aaatgtccaa	gtcccacg	gacagacgct	caaggatcat	tcttacggat	840
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acatatgacc	cagtcgctcg	gcgaatttaa	tagagatcct	gagtcacttc		960
gatggacgaa	cttgcgatga	gattgccatg	gaataccgtt	cagccagtct	tcgcgctcta	1020

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<210> 102

<211> 399

<212> PRT

<213> Aspergillus fumigatus

<220>

<223> Phylum CEA230; clone 9-11; contig 4899 region 9642-7242
Protein sequence

<400> 102

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Glu Val Phe Arg Arg Trp Ser Ser Ser Glu Thr Ala Lys Ser Ser Ser
          35          40          45

Ala Ala Asn Gln Thr Ile Phe Ser Gly Ile Gln Pro Thr Gly Val Pro
          50          55          60

His Leu Gly Asn Tyr Leu Gly Ala Leu Arg Glu Trp Val Arg Leu Gln
65          70          75          80

Asn Ala Ala Lys Glu Gly Thr Arg Leu Phe Phe Ser Ile Val Asp Leu
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His Ala Leu Thr Val Pro Gln Asp Ala Ser Gln Leu Arg Asn Trp Arg
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Lys Glu Thr Phe Ala Thr Leu Ile Ala Val Gly Leu Asp Pro Asn Arg
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Ser Thr Ile Phe Tyr Gln Ser Ala Val His Ala His Ala Glu Leu Phe
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Trp Ile Leu Cys Thr Ile Ala Ser Met Gly Tyr Leu Ser Arg Met Thr
145          150          155          160

Gln Trp Lys Lys Glu Gln Leu Ala Asp Val Gly Gln Ser Lys Leu Gln
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Leu Pro Asp Asn Ala Asn Leu Glu Asp Ser Thr Ala Arg Ser Arg Leu
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Arg Leu Gly Leu Phe Ser Tyr Pro Val Leu Gln Ala Ala Asp Ile Leu
          195          200          205

Ile Arg Ala Thr His Val Pro Val Gly Asp Asp Gln Arg Gln His Leu
          210          215          220

Glu Phe Ser Arg Asn Thr Ala Asn Ser Phe Asn His Val Tyr Gly Pro
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Arg Ser Arg Ile Ile Leu Thr Asp Ser Pro Ala Glu Ile Ser Lys Lys
275 280 285

Ile Asn Ala Ala Leu Thr Asp Ser Glu Leu Thr Ile Thr Tyr Asp Pro
290 295 300

Val Arg Arg Pro Gly Val Ala Asn Leu Ile Glu Ile Leu Ser His Phe
305 310 315 320

Asp Gly Arg Thr Cys Asp Glu Ile Ala Met Glu Tyr Arg Ser Ala Ser
325 330 335

Leu Arg Ala Leu Lys Glu His Leu Ala Arg Thr Leu Ser Asn His Leu
340 345 350

Glu Pro Ile Arg Glu Lys Tyr Leu Ser Leu Val Gly Asp Gln Thr Asp
355 360 365

Tyr Leu Asp Ser Ile Ala Glu Gln Gly Ser Glu Ala Ala Arg Ala Asn
370 375 380

Ala Glu Leu Thr Met Glu Gln Val Lys Val Ala Met Gly Leu Ile
385 390 395

<210> 103

<211> 3805

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA231; clone 10-80; contig 4940 region 54154-50350
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 103

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acagagtttg	ttagctcacc	gcctttggat	tttcaactgt	aaaacaaaaa	aaaagtgaga	240
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<210> 104

<211> 2805

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA231; clone 10-80; contig 4940 region 54154-50350
Genomic sequence containing the coding region

<400> 104

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aatgacgacg aggcctttat tgccgagcag caaacttctg ccaaccgcaa ggctcgaat 240
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<210> 105

<211> 2805

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA231; clone 10-80; contig 4940 region 54154-50350
Coding region without introns

<400> 105

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<210> 106

<211> 934

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA231; clone 10-80; contig 4940 region 54154-50350
Protein sequence

<400> 106

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Pro Ser Ala Lys Ser Lys Arg Gln Pro Pro Lys Lys Val Pro Ser Gln
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PCT/IB03/01374

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 65 70 75 80
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 85 90 95
 Leu Ser Ala Asn Leu Leu Lys Ala Ile Ala Arg Lys Gly Phe Ser Val
 100 105 110
 Pro Thr Pro Ile Gln Arg Lys Thr Ile Pro Val Ile Met Asp Asp Gln
 115 120 125
 Asp Val Val Gly Met Ala Arg Thr Gly Ser Gly Lys Thr Ala Ala Phe
 130 135 140
 Val Ile Pro Met Ile Glu Lys Leu Lys Ser His Ser Thr Lys Val Gly
 145 150 155 160
 Ala Arg Gly Leu Val Leu Ser Pro Ser Arg Glu Leu Ala Leu Gln Thr
 165 170 175
 Leu Lys Val Val Lys Glu Leu Gly Arg Gly Thr Asp Leu Lys Ser Val
 180 185 190
 Leu Leu Val Gly Gly Asp Ser Leu Glu Glu Gln Phe Ala Met Ile Ala
 195 200 205
 Gly Asn Pro Asp Ile Ile Ile Ala Thr Pro Gly Arg Phe Leu His Leu
 210 215 220
 Lys Val Glu Met Asn Leu Asp Leu Ser Ser Ile Arg Tyr Val Val Phe
 225 230 235 240
 Asp Glu Ala Asp Arg Leu Phe Glu Met Gly Phe Ala Ala Gln Leu Thr
 245 250 255
 Glu Ile Leu His Gly Leu Pro Ala Asn Arg Gln Thr Leu Leu Phe Ser
 260 265 270
 Ala Thr Leu Pro Lys Ser Leu Val Glu Phe Ala Arg Ala Gly Leu Gln
 275 280 285
 Glu Pro Thr Leu Val Arg Leu Asp Thr Glu Ser Lys Ile Ser Pro Asp
 290 295 300
 Leu Gln Asn Ala Phe Phe Ser Val Lys Ser Ser Glu Lys Glu Gly Ala
 305 310 315 320
 Leu Leu Tyr Ile Leu His Glu Val Ile Lys Met Pro Thr Gly Pro Thr
 325 330 335
 Glu Val Ser Gln Gln Arg Lys Glu Glu Asp Ala Ser Ala Lys Asn Leu
 340 345 350
 Lys Asn Lys Lys Arg Lys Arg Ala Glu Met Glu Lys Ala Val Asn Thr
 355 360 365

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Arg Glu Ser Pro Thr Lys His Ser Thr Ile Val Phe Ala Ala Thr Lys
 370 375 380
 His His Val Asp Tyr Leu Tyr Ser Leu Leu Cys Glu Ala Gly Phe Ala
 385 390 395 400
 Val Ser Tyr Val Tyr Gly Ser Leu Asp Gln Thr Ala Arg Lys Ile Gln
 405 410 415
 Val Gln Asn Phe Arg Thr Gly Met Thr Asn Ile Leu Val Val Thr Asp
 420 425 430
 Val Ala Ala Arg Gly Ile Asp Ile Pro Ile Leu Ala Asn Val Ile Asn
 435 440 445
 Tyr Asp Phe Pro Ser Gln Pro Lys Ile Phe Val His Arg Val Gly Arg
 450 455 460
 Thr Ala Arg Ala Gly Arg Lys Gly Trp Ser Tyr Ser Leu Val Arg Asp
 465 470 475 480
 Ala Asp Ala Pro Tyr Leu Leu Asp Leu Gln Leu Phe Leu Gly Arg Arg
 485 490 495
 Leu Val Val Gly Arg Glu Phe Gly Asp Gln Val Asn Phe Ala Glu Asp
 500 505 510
 Val Val Thr Gly Ser Leu Pro Arg Asp Gly Leu Ser Gln Ser Cys Glu
 515 520 525
 Trp Val Thr Lys Val Leu Asp Asp Asn Ala Asp Leu Ala Ala Gln Arg
 530 535 540
 Thr Val Ala Ala Lys Gly Glu Lys Leu Tyr Met Arg Thr Arg Asn Ala
 545 550 555 560
 Ala Ser Leu Glu Ser Ala Lys Arg Ser Lys Gln Val Val Ser Ser Asp
 565 570 575
 Asn Trp Thr Ser Val His Pro Leu Phe Gln Asp Glu Thr Ser Asn Leu
 580 585 590
 Glu Ala Glu Arg Glu Lys Met Leu Ala Arg Ile Gly Gly Tyr Arg Pro
 595 600 605
 Pro Glu Thr Ile Phe Glu Val Asn Asn Arg Arg Met Gly Lys His Glu
 610 615 620
 Asn Val Asp Ala Leu Asp Thr Ile Lys Arg Val Arg Ser Thr Leu Glu
 625 630 635 640
 Ser Lys Lys Lys Arg Ala Gln Ala Asn Glu Lys Ser Glu Phe Leu Glu
 645 650 655
 Asp Gly Pro Asp Asp Gly Lys Ala Val Asn Glu Ala Lys Glu Thr Glu
 660 665 670
 Ser Glu Gly Ala Phe Ser Asp Glu Asp Asp Val Pro Thr Gly Val
 675 680 685
 Ala Asp Asn Met Ser Met Ala Ser Asp Ser Glu Leu Glu Val Thr Phe

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690	695	700
Ser Ser Tyr Ser Lys	Ser Lys Asp Asn Lys Ala Lys Lys Ala Ser Ala	
705	710	715 720
Ala Ser Phe Gln Asn Pro Glu Tyr Phe Met Ser Tyr Thr Pro Asn Asn		
	725	730 735
Thr Ser Leu Ala Glu Asp Arg Ala Tyr Gly Val His Ser Gly Thr Asn		
	740	745 750
Ser Asn Phe Ala Gln Ala Ser Arg Ser Ala Thr Met Asp Leu Ala Gly		
	755	760 765
Asp Asp Gly Gly Arg Gly Phe Gly Glu Ala Arg Thr Leu Met Arg Trp		
	770	775 780
Asp Lys Arg His Lys Lys Tyr Val Ala Arg Gln Asn Asp Glu Asp Gly		
	785	790 795 800
Ser Lys Gly Thr Arg Leu Val Arg Gly Glu Ser Gly Ala Lys Ile Ala		
	805	810 815
Ala Ser Phe Arg Ser Gly Arg Phe Asp Ala Trp Lys Arg Glu Asn Arg		
	820	825 830
Leu Gly Arg Leu Pro Arg Val Gly Glu Ala Glu Ala Ala Asn Leu Ala		
	835	840 845
Ala Gly Leu Asn Ala Ala Ile Ser Gly Lys Arg Phe Arg His Arg Lys		
	850	855 860
Glu Gln Ala Pro Lys Lys Ala Asp Pro Leu Arg Gly Asp Tyr Glu Lys		
	865	870 875 880
Met Lys Lys Lys Ala Glu Leu Ala Lys Glu Arg Ala Met Ser Lys Ala		
	885	890 895
Gly Gly Ala Ala Pro Arg Gly Lys Ser Glu Leu Lys Ser Thr Asp Asp		
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Arg Pro Ser Arg Lys Lys		
930		

<210> 107

<211> 2413

<212> DNA

<213> Aspergillus fumigatus

<220>

<223> Phylum CEA232; clone 10-175; contig 4938 region 211008-213420
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 107

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tagtgaatgg gtttagaagt tacagcctag aaatgagagg gaaagagagg tacattgaaa	120
gcaagaagat atggtcggta ttacatcac ctccttctct gccttgagtg cctaccgctc	180

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tgctgcctgc	gtgcccaccg	acttcaccag	tgacgcgacg	tcgtcatcgg	agcaacgcgg	240
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gggtcaaaact	ccagcactgt	tccgtcatca	accacctaag	ggcctagata	tggtctccag	360
ttacagatcc	ttcgtgccac	gattctttca	ttgagtggtc	aaatactact	cgacgtatatt	420
ttgtgggctt	cagtttggtg	ctaattgttag	accgatagac	gacggccaac	ctttttaata	480
cactatcatc	gcacctcccc	atggctctcc	gccggccatt	aacacttccg	aggcacattc	540
tcaatggagc	ttgttttaggc	ttgcgaccag	ctgtgtctcg	cgcgcctctg	gcttatgggc	600
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ccaaaggccc	cacggcaatg	gtcttctctca	acatgggtgg	gccatcgaag	attgacgaag	720
tggaagattt	tctgagcaga	ttattttgat	gcattcctca	atatgccoga	tgctaccacc	780
atgtatgagt	ctgacaaaact	ctctcttctct	ataccaggcc	gatggcgatc	tgattcctct	840
oggacgactt	caatcatatac	tcggccctct	catcgctaag	cgcagaacct	caaagatcca	900
acggcaatac	tcggatatattg	gtggagggtc	accgatcagg	aaatgggtccg	agtatcagtg	960
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taagcgtgca	aatggcaaca	tggaacccgc	tggtgccatc	cagtggagtg	tcattgatcg	1260
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gagagaagtg	ctcactacag	atgactctgc	gctgtcaagg	ctgtaagagc	gaacggtgcc	1860
tggaacagaa	gaaattcttt	gctggcgacc	gattttcttc	tcttgtagtt	tagtgtatatt	1920
ctatatggct	gttctctgcc	gttgatataca	atactagggg	ccattttctt	tcttcagggc	1980
gttaagtgtg	gttgtcaacg	aggtgaccca	ttcacggagc	acagcagagc	aatgtatata	2040
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atataaaatc	attaggaatg	aaggatttcc	gggtcaacct	ttgacaatta	ttttgccacc	2160
atttaacgtt	gcacatatgc	aacgataaag	cacgacccag	tcgtagtgtt	ggtgtccctt	2220
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ttgattattg	aacaaaactct	catagcgtcg	tttcgtaatt	actggttggt	cggaatcggg	2340
ctgacgcaaa	gccccacggc	cacgaagctg	ctccagctcc	gttcccagtt	ctcgtgaaga	2400
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<210> 108

<211> 1413

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA232; clone 10-175; contig 4938 region 211008-213420
Genomic sequence containing the coding region

<400> 108

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gcaacagcag	ttcccccggt	cactcaaaat	gcggctgggt	ccaaaggccc	cacggcaatg	180
gtcttctctca	acatgggtgg	gccatcgaag	attgacgaag	tggaagattt	tctgagcaga	240
ttattttgat	gcattcctca	atatgcccgga	tgctaccacc	atgtatgagt	ctgacaaaact	300
ctctcttctct	ataccaggcc	gatggcgatc	tgattcctct	cggacgactt	caatcatacc	360
tcggccctct	catcgctaag	cgcagaacct	caaagatcca	acggcaatac	tcggatatattg	420
gtggagggtc	accgatcagg	aaatgggtccg	agtatcagtg	cgaggaaatg	tgacagattgc	480
tagacaaaaat	caatccccgaa	acggctcctc	acaagcctta	cgctcgcttc	cggtacgccg	540
accctctgac	ggaaagaaatg	tacacaaagt	tgctggaaga	tggtattcggc	aacgggaaag	600
gcggggcgcg	tgctcgcttc	acacagtacc	cccaatattc	gtgctccacc	acgggttagct	660

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cgctgaacga gttgtggaaa tggagaacca ggcttgaggg taagcgtgca aatggcaaca 720
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tcgtggaggc ttctgcccgg aacattgagg agcagctgaa gacataccca gaggagaagc 840
gaaacgggtg cgttctcttg ttctcagccc acagctctgcc catgagtgtt gtcaacagag 900
gtgagactca tcttcttacc gaacaacaag atttgcctgc taacacattt cctaggcgac 960
ccatatacctg ctgaagttgc tgcaactgtg catgctgtca tgcaaagatt gaatttcagc 1020
aatccttacc gactgtgctg gcagtcctca gtgggaccgt cagcttggct tggagcccaa 1080
actagcgata cggtcgaaaa ctatgtcaaa cgtggacaga ccgatattat tctagttccc 1140
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gaagcaaact ccccgagggt caagagagcc gagagtgtga atggttaacc cattttcatt 1260
caggcattag cagacattgc ccaagagcac ctccgtaagg gagagaagtg ctcactacag 1320
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gctggcgacc gatcttcttc tctttagttag tag 1413

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<210> 109

<211> 1287

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA232; clone 10-175; contig 4938 region 211008-213420
Coding region without introns

<400> 109

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ttgcgaccag ctgtgtctcg cgcgcgtctg gcttatgggc aggagcagag gaaagggcct 120
gcaacagcag ttcccccggt cactcaaaat gcggctgggt ccaaaggccc cacggcaatg 180
gtcttctctca acatgggtgg gccatcgaag attgacgaag tggaaagatt tctgagcaga 240
ttatttgccg atggcgatct gattcctctc ggacgacttc aatcatacct cggccctctc 300
atcgctaagc gcagaacccc aaagatccaa cggcaatact cggatattgg tggagggtca 360
ccgatcagga aatgggtccga gtatcagtg caggaaatgt gcagattgct agacaaaatc 420
aatcccgaaa cggctcctca caagccttac gtcgcgttcc ggtacgccga ccctctgacg 480
gaagaaatgt acacaaaagt gctggaagat ggattcggca acgggaaagg cgggcgcgct 540
gtcgcgttca cacagtaccc ccaatattcg tgcctcacca cgggtagctc gctgaacgag 600
ttgtgaaaat ggagaaccag ccttgagggt aagcgtgcaa atggcaacat ggaccccgct 660
ggtgccatcc agtggagtg cattgatcga tggccaacgc accctggcct cgtggaggct 720
ttcgcgccga acattgagga gcagctgaag acatacccag aggagaagcg aaacggtgtc 780
gttctcttgt tctcagccca cagtctgccc atgagtgttg tcaacagagg cgacccatat 840
cctgctgaag ttgctgcaac tgtgcatgct gtcctgcaaa gattgaattt cagcaatcct 900
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gatacggctc aaaactatgt caaacgtgga cagaccgata ttattctagt tcccattgcc 1020
ttcaccagcg accatattga gactctgtac gagttggatc tggaaagtga aaaggaagca 1080
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ttagcagaca ttgcccaaga gcacctccgt aaggagaga agtgctcact acagatgact 1200
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gaccgatttt cttctcttgt agtttag 1287

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<210> 110

<211> 428

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA232; clone 10-175; contig 4938 region 211008-213420
Protein sequence

<400> 110

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Met Ala Leu Arg Arg Pro Leu Thr Leu Pro Arg His Ile Leu Asn Gly
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Ala Cys Leu Gly Leu Arg Pro Ala Val Ser Arg Ala Ala Leu Ala Tyr
 20 25 30
 Gly Gln Glu Gln Arg Lys Gly Leu Ala Thr Ala Val Pro Pro Val Thr
 35 40 45
 Gln Asn Ala Ala Gly Ser Lys Gly Pro Thr Ala Met Val Phe Leu Asn
 50 55 60
 Met Gly Gly Pro Ser Lys Ile Asp Glu Val Glu Asp Phe Leu Ser Arg
 65 70 75 80
 Leu Phe Ala Asp Gly Asp Leu Ile Pro Leu Gly Arg Leu Gln Ser Tyr
 85 90 95
 Leu Gly Pro Leu Ile Ala Lys Arg Arg Thr Pro Lys Ile Gln Arg Gln
 100 105 110
 Tyr Ser Asp Ile Gly Gly Gly Ser Pro Ile Arg Lys Trp Ser Glu Tyr
 115 120 125
 Gln Cys Glu Glu Met Cys Arg Leu Leu Asp Lys Ile Asn Pro Glu Thr
 130 135 140
 Ala Pro His Lys Pro Tyr Val Ala Phe Arg Tyr Ala Asp Pro Leu Thr
 145 150 155 160
 Glu Glu Met Tyr Thr Lys Leu Leu Glu Asp Gly Phe Gly Asn Gly Lys
 165 170 175
 Gly Gly Arg Ala Val Ala Phe Thr Gln Tyr Pro Gln Tyr Ser Cys Ser
 180 185 190
 Thr Thr Gly Ser Ser Leu Asn Glu Leu Trp Lys Trp Arg Thr Arg Leu
 195 200 205
 Glu Gly Lys Arg Ala Asn Gly Asn Met Asp Pro Ala Gly Ala Ile Gln
 210 215 220
 Trp Ser Val Ile Asp Arg Trp Pro Thr His Pro Gly Leu Val Glu Ala
 225 230 235 240
 Phe Ala Arg Asn Ile Glu Glu Gln Leu Lys Thr Tyr Pro Glu Glu Lys
 245 250 255
 Arg Asn Gly Val Val Leu Leu Phe Ser Ala His Ser Leu Pro Met Ser
 260 265 270
 Val Val Asn Arg Gly Asp Pro Tyr Pro Ala Glu Val Ala Ala Thr Val
 275 280 285
 His Ala Val Met Gln Arg Leu Asn Phe Ser Asn Pro Tyr Arg Leu Cys
 290 295 300
 Trp Gln Ser Gln Val Gly Pro Ser Ala Trp Leu Gly Ala Gln Thr Ser
 305 310 315 320
 Asp Thr Val Glu Asn Tyr Val Lys Arg Gly Gln Thr Asp Ile Ile Leu
 325 330 335

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PCT/IB03/01374

Val Pro Ile Ala Phe Thr Ser Asp His Ile Glu Thr Leu Tyr Glu Leu
 340 345 350

Asp Leu Glu Val Ile Lys Glu Ala Asn Ser Pro Gly Val Lys Arg Ala
 355 360 365

Glu Ser Leu Asn Gly Asn Pro Ile Phe Ile Gln Ala Leu Ala Asp Ile
 370 375 380

Ala Gln Glu His Leu Arg Lys Gly Glu Lys Cys Ser Leu Gln Met Thr
 385 390 395 400

Leu Arg Cys Gln Gly Cys Lys Ser Glu Arg Cys Leu Glu Gln Lys Lys
 405 410 415

Phe Phe Ala Gly Asp Arg Phe Ser Ser Leu Val Val
 420 425

<210> 111

<211> 2865

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA233; clone 10-290; contig 4865 region 3495-6359
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 111

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acaaggcggg	atcgtctttc	aacacgcggg	cggtgagctt	atcagcgccg	attgcggggg	180
ggtgcagcaa	atcaagtcag	tcgccacttt	cggcgacccat	gacaaagcgc	aagattggct	240
ttactaaacc	gcctactttt	tttttatcaa	agagacttgg	gtttgtcagc	ttttctttat	300
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tttgtcgta	ttttcgctcg	attgcatcta	caacaaagaa	aacgggctcg	acgaaccctg	420
cgagatccat	acttcctggg	gtggcggtct	tcttagtctt	tatcgcatag	cggggtgctc	480
gaccagaagt	ccctgccacg	atgagtgcaa	tcctttctgc	agacgatttg	aacgatttca	540
tttctcccg	ggttgcttgc	atcaagcccg	ttgagagtct	accacaaaaa	gaatcccagt	600
cggaggtatc	tttctgtctt	taccagtcct	ctgttgatat	cagccaatag	gctaacgctc	660
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gggccctcac	ggtctcagag	ctggtggaaa	acatggcaat	gggtttacat	gggttgtgga	1080
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ctggatatgt	tatgctgaaa	aaacacaccc	ttttatcctt	ccgcatttat	ctcgcttcaa	1260
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acaaaatctc	gtcagaaaac	ttaaaccgcg	acgcgtgtca	agactgccag	gcgccaagcc	1860
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tggaacaggc	gctgattatg	catatgttga	agtcattggc	tgtcctggcg	gctgtaccaa	1980
tggtggtggg	caaataagga	ttgaagatgc	ccgggaggct	gttccgaacg	cactaaaaga	2040
gacatcgact	gaaactcctg	tggtcgcacc	gaaacccacg	ccgcatgagc	agcgtgcctg	2100
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attctctcca	acaactcgcc	ttcaatcacc	cacgccccag	tttat		2865

<210> 112

<211> 1865

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA233; clone 10-290; contig 4865 region 3495-6359
 Genomic sequence containing the coding region

<400> 112

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cctatgaggt	gacaaaaggaa	gacaaaagttc	aaccggaaaa	ccttcccccg	gctcagattt	240
cattgactga	ttgccttgca	tgtctccggat	gtgtcacgtc	tgcggaagca	gtgttgatat	300
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gttctacaag	ctaccaaaaga	ggcacacaaa	aagttggatc	agcagacagc	gatggtcgca	420
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gccttcccaa	gagtcgaatt	ctttcgtccg	cttgcgccgg	ctggatatgt	tatgtctgaa	720
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gcacatttct	gaagtcagtg	ctaagcaagg	cacttggggg	cccgccttct	cagatatggc	840
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gtgtcataac	caccgcgtgag	ctactaactt	tagccactgc	tagggggctt	tctctaccca	1020
atttgccgct	caaaccattg	cccgcgtcat	gtttaactcc	atttccagat	caagccctag	1080
aatcattttt	gttctctaag	agctcgtcgg	gccaaacagt	cgaatcaggg	acatctggag	1140
gctatcttca	tcacgtcttc	caaactcttc	aagccagaaa	ccccggcagc	aagattgtca	1200
cccagcgtgg	gcgcaacgcc	gatgttgtgg	aatatgtgct	catgtcgtct	ggggatgagc	1260
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caaatcgacg	acagcccattg	tcaaggaacg	cagctccggc	tggaaacaggc	gctgattatg	1440
catatgttga	agtcattggc	tgtcctggcg	gctgtaccaa	tggtggtggg	caaataagga	1500
ttgaagatgc	ccgggaggct	gttccgaacg	cactaaaaga	gacatcgact	gaaactcctg	1560
tggtcgcacc	gaaacccacg	ccgcatgagc	agcgtgcctg	gctagcccgg	gtagatgaag	1620
cgtactactc	tgcggactcg	gatagcgagg	gatctgtcac	gacggagccg	gtttctgtcc	1680
tgtcaaggga	taaccagatt	catgagtttt	tgaactattg	gtcagagaag	gttgatatac	1740
ccctttcccg	gctcgcgtac	acgtcctatc	gcgaagtggg	gagcgacgtg	ggtaagacga	1800
agaatgcggc	caacgaaact	gctcgtgttg	tggaaattggc	aggaaagatc	ggaggtgggt	1860
ggtga						1865

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<210> 113
 <211> 1725
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA233; clone 10-290; contig 4865 region 3495-6359
 Coding region without introns

<400> 113
 atgagtgcaa tcctttctgc agacgatttg aacgatttca tttctcccgg gggtgcttgc 60
 atcaagcccc ttgagagtct accacaaaaa gaatcccagt cggagaatcc ctatgagggtg 120
 acaaaggaag acaaagtcca accggaaaac cttccccccg ctcagatttc attgactgat 180
 tgccttgcat gctccggatg tgtcacgtct gcggaagcag tgttgatatc cttgcaatca 240
 catacggagg ttctcaatac tcttgattcc gatggtcgca tctttgttgc tagcgtcagc 300
 cctcaagtca gggcgagctt ggcagccaca tacggaatca ccgagcggga ggcgaaatat 360
 atgattgacc aatttcttat gggccctcac ggtctcagag ctggtggaaa acatggcaat 420
 gggtttacat gggttggtga cacgaacgtt atgctgaag cagtgttggc tctgacagcg 480
 gacgaggtca cgagctcttt attatcaact ggatcgggca gccttcccaa gagtccaatt 540
 ctttctgccc ctgtccccgg ctggatatgt tatgctgaaa aaacacaccc ttttatcctt 600
 ccgcatttat ctgcctcaa gtctcctcag gcgttgagcg gcacatttct gaagtcagtg 660
 ctaagcaagg cacttggggt cccgccttct cagatatggc atttagctat catgccatgc 720
 ttcgacaaga agctggaagc tagccgggaa gagctgacag acattgcatg ggcttcaacc 780
 ttcacccagt cacagacaac acccgtccgc gacgttgact gtgtcataac caccgtgag 840
 ctactaactt tagccactgc tagggggctt tctctaccca atttgccgct caaaccattg 900
 ccgcgctcat gtttaactcc atttccagat caagccctag aatcattttt gttctctaag 960
 agctcgtcgg gccaaacagt cgaatcaggg acatctggag gctatcttca tcacgtcctc 1020
 caaatcttcc aagccagaaa ccccggcagc aagattgtca ccagcgtgg gcgcaacgcc 1080
 gatgttggtg aatatgtgct catgtcgtct ggggatgagc ctctttttag ggcggtcgg 1140
 tattatggct tcaggaatat acaaaatctc gtcagaaaac ttaaaccgcg acgcgtgtca 1200
 agactgccag gcgccaagcc gcaagcggtc tcttcaagtg caaatcgacg acagcccatg 1260
 tcaaggaacg cagctccggc tggaaacaggc gctgattatg catatgttga agtcatggct 1320
 tgtcctggcg gctgtaccaaa tgggtgggtgg caaataagga ttgaagatgc ccgggagggt 1380
 gttccgaacg cactaaaaga gacatcgact gaaactcctg tggctgcacc gaaaccacg 1440
 ccgcatgagc agcgtgcctg gtagcccggt gtagatgaag cgtactactc tgcggactcg 1500
 gatagcgagg gatctgtcac gacggagccg gtttctgtcc tgtcaaggga taaccagatt 1560
 catgagtttt tgaactattg gtcagagaag gttgatatac ccctttcccg gctcgcgtac 1620
 acgtcctatc gcgaagtga gagcgacgtg ggtaagacga agaatgcgcc caacgaaact 1680
 gctcgtgttg tgaattggc aggaagatc ggaggtggtt ggtga 1725

<210> 114
 <211> 574
 <212> PRT
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA233; clone 10-290; contig 4865 region 3495-6359
 Protein sequence

<400> 114

Met Ser Ala Ile Leu Ser Ala Asp Asp Leu Asn Asp Phe Ile Ser Pro
 1 5 10 15

Gly Val Ala Cys Ile Lys Pro Val Glu Ser Leu Pro Gln Lys Glu Ser
 20 25 30

Gln Ser Glu Asn Pro Tyr Glu Val Thr Lys Glu Asp Lys Val Gln Pro
 35 40 45

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Glu Asn Leu Pro Pro Ala Gln Ile Ser Leu Thr Asp Cys Leu Ala Cys
 50 55 60
 Ser Gly Cys Val Thr Ser Ala Glu Ala Val Leu Ile Ser Leu Gln Ser
 65 70 75 80
 His Thr Glu Val Leu Asn Thr Leu Asp Ser Asp Gly Arg Ile Phe Val
 85 90 95
 Ala Ser Val Ser Pro Gln Val Arg Ala Ser Leu Ala Ala Thr Tyr Gly
 100 105 110
 Ile Thr Glu Arg Glu Ala Lys Tyr Met Ile Asp Gln Phe Leu Met Gly
 115 120 125
 Pro His Gly Leu Arg Ala Gly Gly Lys His Gly Asn Gly Phe Thr Trp
 130 135 140
 Val Val Asp Thr Asn Val Met Arg Glu Ala Val Leu Ala Leu Thr Ala
 145 150 155 160
 Asp Glu Val Thr Ser Ser Leu Leu Ser Thr Gly Ser Gly Ser Leu Pro
 165 170 175
 Lys Ser Pro Ile Leu Ser Ser Ala Cys Pro Gly Trp Ile Cys Tyr Ala
 180 185 190
 Glu Lys Thr His Pro Phe Ile Leu Pro His Leu Ser Arg Leu Lys Ser
 195 200 205
 Pro Gln Ala Leu Ser Gly Thr Phe Leu Lys Ser Val Leu Ser Lys Ala
 210 215 220
 Leu Gly Val Pro Pro Ser Gln Ile Trp His Leu Ala Ile Met Pro Cys
 225 230 235 240
 Phe Asp Lys Lys Leu Glu Ala Ser Arg Glu Glu Leu Thr Asp Ile Ala
 245 250 255
 Trp Ala Ser Thr Phe Thr Gln Ser Gln Thr Thr Pro Val Arg Asp Val
 260 265 270
 Asp Cys Val Ile Thr Thr Arg Glu Leu Leu Thr Leu Ala Thr Ala Arg
 275 280 285
 Gly Leu Ser Leu Pro Asn Leu Pro Leu Lys Pro Leu Pro Ala Ser Cys
 290 295 300
 Leu Thr Pro Phe Pro Asp Gln Ala Leu Glu Ser Phe Leu Phe Ser Lys
 305 310 315 320
 Ser Ser Ser Gly Gln Thr Val Glu Ser Gly Thr Ser Gly Gly Tyr Leu
 325 330 335
 His His Val Leu Gln Ile Phe Gln Ala Arg Asn Pro Gly Ser Lys Ile
 340 345 350
 Val Thr Gln Arg Gly Arg Asn Ala Asp Val Val Glu Tyr Val Leu Met
 355 360 365

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Ser Ser Gly Asp Glu Pro Leu Phe Arg Ala Ala Arg Tyr Tyr Gly Phe
 370 375 380

Arg Asn Ile Gln Asn Leu Val Arg Lys Leu Lys Pro Ala Arg Val Ser
 385 390 395 400

Arg Leu Pro Gly Ala Lys Pro Gln Ala Val Ser Ser Ser Ala Asn Arg
 405 410 415

Arg Gln Pro Met Ser Arg Asn Ala Ala Pro Ala Gly Thr Gly Ala Asp
 420 425 430

Tyr Ala Tyr Val Glu Val Met Ala Cys Pro Gly Gly Cys Thr Asn Gly
 435 440 445

Gly Gly Gln Ile Arg Ile Glu Asp Ala Arg Glu Ala Val Pro Asn Ala
 450 455 460

Leu Lys Glu Thr Ser Thr Glu Thr Pro Val Ala Ala Pro Lys Pro Thr
 465 470 475 480

Pro His Glu Gln Arg Ala Trp Leu Ala Arg Val Asp Glu Ala Tyr Tyr
 485 490 495

Ser Ala Asp Ser Asp Ser Glu Gly Ser Val Thr Thr Glu Pro Val Ser
 500 505 510

Val Leu Ser Arg Asp Asn Gln Ile His Glu Phe Leu Asn Tyr Trp Ser
 515 520 525

Glu Lys Val Asp Ile Pro Leu Ser Arg Leu Ala Tyr Thr Ser Tyr Arg
 530 535 540

Glu Val Glu Ser Asp Val Gly Lys Thr Lys Asn Ala Pro Asn Glu Thr
 545 550 555 560

Ala Arg Val Val Glu Leu Ala Gly Lys Ile Gly Gly Gly Trp
 565 570

<210> 115

<211> 1510

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA234; clone 10-304; contig 4899 region 443110-444619

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 115

taagagttgc	aggtatgagc	ctggtaaatac	aagtcagtc	cggatagcac	aacagaacct	60
cattttgtcc	tgaaagaatg	aacaaaaagg	ccaactcaga	ctctttgcaa	atgcaaggaa	120
gaggtaatga	gaatgttttg	ggagaagctt	aaatgtagct	ttgccggaac	ggagaattga	180
gtaaagccgg	tcatgaggcg	ccaagacccc	agcgaaaaag	cagccctagg	ccgcacgcaa	240
ccccgttcgg	cgagttgcta	ctggctgtta	agcgagactc	ttgtgggcga	agaccgcaac	300
acccgaaatt	cgcgatccag	tagcccagag	cgacttggtg	gcgtttcggg	cgactttgac	360
aatcccgaact	cttcgacaac	aaattcccat	caccgccctc	ccggagtctg	tcgaccgtga	420
gtttgaaacc	tacgccctat	cgaatttctg	gactgtcact	gaagaatccg	tttttgtcgt	480
tttttttagga	agccttcgac	atggccgata	tcgatgtcaa	ggttgctcaa	tggaagcttg	540
ttgaggttgg	ccgtgtttgt	ctgatccgca	gcgggtccta	caccggcaag	cttgctgcca	600
ttgtcgagat	catcgaccac	aagcgtgtac	gtttttcaac	ggagaaattc	tgagcgagag	660

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```

acggaaagat catggtcggg tgtgatattg acaaagaggc gcgatcatag gtcctggttg 720
acggtccttc caccgaggag aacaagatcg ttccccgtca cgctcttctt ctcgctcacg 780
ccactctcac ccccttcgtc attcccaaac tcccccgcg tgccggcact ggccccgtca 840
agaagctctg ggagaagaac gagatcgatg gaaagtgggc taagagcacc attgctcaga 900
agactgagcg cgctgagcgg aggaagaacc ttaccgactt cgagcgcttc aaggtcctca 960
gactcaagaa gcaggtacgt tcagtttgcg aaactatggg agaattgtga tggcacattg 1020
gagggcattc ttggcaactc tgcactcgct ttccgcgaga gggaagagga gcaattactt 1080
gtattatgat ttgcgactgg ttactgacat ctggtgattt aacaggctcg ctacgaggtc 1140
cagaaggctc acgccaaagg cagggctgct gtcctaagt catagatgtt ttcattgaggc 1200
tcggtgcata gtatgaaggg gtaccttggg acggttttac atggctgagg gttttattct 1260
atcttcagaa aaattaagct gtatccacta caatgacagc caaaaaatga ttcaaacctt 1320
tgatatcctg acacgggtca tctgtctatg tcactcagatt cgcgaccccg attagtactt 1380
ggctctgggt tatagccgtc tccttagaca ttaattggga attaaacatt ttagactcaa 1440
gatcacggaa tatgtaagaa agtatcgtaa tgtacattac tgagtggat tggctcgtaa 1500
tgactcgtaa 1510

```

<210> 116

<211> 685

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA234; clone 10-304; contig 4899 region 443110-444619
Genomic sequence containing the coding region

<400> 116

```

atggccgata tcgatgtcaa ggttgctcaa tggaaagcttg ttgaggttg ccgtgtgtg 60
ctgatccgca gcggtcctta caccggcaag cttgctgcca ttgtcgagat catcgaccac 120
aagcgtgtac gtttttcaac ggagaaattc tgagcgcagg acggaaagat catggtcggg 180
tgtgatattg acaaagaggc gcgatcatag gtcctggttg acggtccttc caccgaggag 240
aacaagatcg ttccccgtca cgctcttctt ctcgctcacg ccactctcac ccccttcgtc 300
attcccaaac tcccccgcg tgccggcact ggccccgtca agaagctctg ggagaagaac 360
gagatcgatg gaaagtgggc taagagcacc attgctcaga agactgagcg cgctgagcgg 420
aggaagaacc ttaccgactt cgagcgcttc aaggtcctca gactcaagaa gcaggtacgt 480
tcagtttgcg aaactatggg agaattgtga tggcacattg gagggcattc ttggcaactc 540
tgcactcgct tttcgcgaga gggaagagga gcaattactt gtattatgat ttgcgactgg 600
ttactgacat ctggtgattt aacaggctcg ctacgaggtc cagaaggctc acgccaaagg 660
cagggctgct gtcctaagt catag 685

```

<210> 117

<211> 465

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA234; clone 10-304; contig 4899 region 443110-444619
Coding region without introns

<400> 117

```

atggccgata tcgatgtcaa ggttgctcaa tggaaagcttg ttgaggttg ccgtgtgtg 60
ctgatccgca gcggtcctta caccggcaag cttgctgcca ttgtcgagat catcgaccac 120
aagcgtgtcc tggttgacgg tccttccacc gaggagaaca agatcggtcc ccgtcacgct 180
cttctctcgc ctcacgccac tctcaccccc ttctgctatt ccaaaactcc ccgcgctgcc 240
ggcactggcc ccgtcaagaa gctctgggag aagaacgaga tcgatggaaa gtgggctaag 300
agcaccattg ctcagaagac tgagcgcgct gagcggagga agaaccttac cgacttcgag 360
cgcttcaagg tcctcagact caagaagcag gctcgtacg aggtccagaa ggctcacgcc 420
aaggtcaggg ctgctgctcc taagtcatag atgttttcat gaggc 465

```

<210> 118

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<211> 149
 <212> PRT
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA234; clone 10-304; contig 4899 region 443110-444619
 Protein sequence

<400> 118

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Met Ala Asp Ile Asp Val Lys Val Ala Gln Trp Lys Leu Val Glu Val
1           5           10           15
Gly Arg Val Val Leu Ile Arg Ser Gly Pro Tyr Thr Gly Lys Leu Ala
          20           25           30
Ala Ile Val Glu Ile Ile Asp His Lys Arg Val Leu Val Asp Gly Pro
          35           40           45
Ser Thr Glu Glu Asn Lys Ile Val Pro Arg His Ala Leu Pro Leu Ala
          50           55           60
His Ala Thr Leu Thr Pro Phe Val Ile Pro Lys Leu Pro Arg Ala Ala
          65           70           75           80
Gly Thr Gly Pro Val Lys Lys Leu Trp Glu Lys Asn Glu Ile Asp Gly
          85           90           95
Lys Trp Ala Lys Ser Thr Ile Ala Gln Lys Thr Glu Arg Ala Glu Arg
          100          105          110
Arg Lys Asn Leu Thr Asp Phe Glu Arg Phe Lys Val Leu Arg Leu Lys
          115          120          125
Lys Gln Ala Arg Tyr Glu Val Gln Lys Ala His Ala Lys Val Arg Ala
          130          135          140
Ala Ala Pro Lys Ser
145

```

<210> 119
 <211> 1942
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA254; clone 7-1-10; contig 4911 region 43163-41221
 Genomic sequence containing 3' and 5'-ends and the coding region

```

<400> 119
tacacccagc acacctaccc tagccacaga tttcttggac cacgggaacc cgaacaaaga      60
gtctctggcc gaactctggt ctaatttcct agagcaggag tcacaggcca gtgggaatcc      120
agaatcgccg aaaccatgaa gagtttcaaa aggtggctct gttctgagcc gtatagaaaa      180
ctagcatctt ctctaagata cggtggttcc acatttatat atgcttgccg actggctttg      240
gtctctctt cttttccatt ctgacttgc ttcgtagtaa taacactgat atcacccgcg      300
tgtttgcgac ttttgcacaa aaccagcttc cccaccgctt tctttctgcc accatagcgg      360
gggacctcgt tattgagcgg acaagtcgtc gttggctttt tctgcacggt tggcctatgc      420
ttcgtttatt cagctctggt acagctggga agttgactga tacactctcc tctctgattt      480
cttggttact cagattgaca atgactaccg gggctggtac gatctctcat tccaacacct      540
atcatcgtat tcctcgccgt taactgacca atccaccagt gcaaagggtt cgtccagtgg      600
tggtatcggg tccctctggg actgggaagt cgaccttgct caagagactc ttcgctgaat      660

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PCT/IB03/01374

```

acccccgatac tttcgattta tccgtgtctc gtacgtctaa ccccttgcca accctcattg 720
actatgcctg cgaattgttt cttttggttg aattgcgctg aacggtgttt gttatatatta 780
gataccactc gagctccccg tcccggggaa gaaaatggac gtgagtatta cttcacaact 840
aaagaagatt tcttgatct tgtgagcaag aatgccttta tcgagcatgc gcagtttggt 900
ggcaattact acggtactac tgtgcaggca gtgaaggatg ttgcgcagaa gggcaagatc 960
tgcgttctcg acattgagat gaggtataaa tagtcctgca acgtgaactg atatgaccgg 1020
agaagcagag gaaatccatc atcaaatgga ttgtagtcca acccaaaca cagctgacga 1080
ctgaattgca atagggcgtg aaacaagtca agcgcaccga tcttgatgct cgattcttat 1140
ttttagcacc cccgtccctt gaagaactag agaaaagact gcgtgggaga gcaaccgaga 1200
ctgaggagag cttgacggta tggctgtcct ccacattcct tcaactcccc aactcgccag 1260
actgtcccg cgggaattcta actttgcgtc agaaacgcct tgcccaagct aaaaatgaat 1320
tggaaatatgc ggcgcagcct ggctctcatg ataagattgt cgtgaacgat gacctggaga 1380
aggcttataa ggaactgcgg gattggattg tcgacggtgg taactttgga gcgcgtcaat 1440
gatttattgg gcatgtctcg gcgtgtttta tttatcagcg ctgctgtata ctttagcgcc 1500
cgtagatact gtcggttgcg atactgaaaa caatgcatca tctgccttgg taacttcggt 1560
ccacagaaac ccataatcaa ggagtcctt tcgtcgtcga cgaacataag agagattaat 1620
tacaatgaaca tcaagactat gctaacaatt cgaatgttgg tctcttttct gtctggagac 1680
gacaaatcta ggaaagggtg tagactcagt cactctcttg aacggagagg agaaaattaa 1740
gcaaaactaa aaaagagaac aaagtctgat gagcaatatg agggctgaaa aggatatctg 1800
taaagaggct gctagaataa aatggaagat gccgattgag aaggcaatgg aggaagagaa 1860
ggggtcattt atcgcagttt gggcgtggac cagaaatgac tgcagtatgt ttatggacca 1920
tgccagccgg agctattgga ct

```

<210> 120

<211> 943

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA254; clone 7-1-10; contig 4911 region 43163-41221
Genomic sequence containing the coding region

<400> 120

```

atgactaccg gggctggtac gatctctcat tccaacacct atcatcgtat tccctgccgt 60
taactgacca atccaccagt gcaaaggttc cgtccagtgg tggatcggg tccctctggg 120
actgggaagt cgaccttgct caagagactc ttcgctgaat accccgatac tttcgattta 180
tccgtgtctc gtacgtctaa ccccttgcca accctcattg actatgcctg cgaattgttt 240
cttttggttg aattgcgctg aacggtgttt gttatatatta gataccactc gagctccccg 300
tcccggggaa gaaaatggac gtgagtatta cttcacaact aaagaagatt tcctggatct 360
tgtgagcaag aatgccttta tcgagcatgc gcagtttggt ggcaattact acggtactac 420
tgtgcaggca gtgaaggatg ttgcgcagaa gggcaagatc tgcgttctcg acattgagat 480
ggaggtaata atagtcctgc aacgtgaact gatatgaccg gagaagcaga ggaaatccat 540
catcaaatgg attgtagttc aacccaaaca acagctgacg actgaattgc aatagggcgt 600
gaaacaagtc aagcgcaccg atcttgatgc tcgattctta ttttagcac ccccgtcctt 660
tgaagaacta gagaaaagac tgcgtgggag agcaaccgag actgaggaga gcttgacggg 720
atggctgtcc tccacattcc ttcacttccc caactcgcca gactgtcccg ctggaattct 780
aactttgcgt cagaaacgcc ttgcccaagc taaaaatgaa ttggaatatg cggcgcagcc 840
tggctctcat gataagattg tcgtgaacga tgacctggag aaggcttata aggaactgcg 900
ggattggatt gtcgacgggt gtaactttgg agcgcgtcaa tga

```

<210> 121

<211> 603

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA254; clone 7-1-10; contig 4911 region 43163-41221
Coding region without introns

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```

<400> 121
atgactaccg gggctgtgca aagggttccgt ccagtggtgg tatcgggtcc ctctgggact    60
gggaagtcga ccttgctcaa gagactcttc gctgaatacc ccgatacttt cgatttatcc    120
gtgtctcata ccaactcgagc tccccgtccc ggggaagaaa atggacgtga gtattacttc    180
acaactaaag aagatttcct ggatcttgtg agcaagaatg cctttatcga gcatgcgag    240
tttggtggca attactacgg tactactgtg caggcagtga aggatgttgc gcagaagggc    300
aagatctgcg ttctcgacat tgagatggag ggcgtgaaac aagtcaagcg caccgatctt    360
gatgctcgat tcttattttt agcaccctcg tcccttgaag aactagagaa aagactgcgt    420
gggagagcaa ccgagactga ggagagcttg acgaaacgcc ttgcccaagc taaaaatgaa    480
ttggaatatg cggcgcgagcc tggctctcat gataagattg tcgtgaacga tgacctggag    540
aaggcttata aggaactgcg ggattggatt gtcgacggtg gtaactttgg agcgcgtcaa    600
tga                                                    603

```

<210> 122

<211> 200

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA254; clone 7-1-10; contig 4911 region 43163-41221
Protein sequence

<400> 122

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Met Thr Thr Gly Ala Val Gln Arg Phe Arg Pro Val Val Val Ser Gly
1          5          10          15

Pro Ser Gly Thr Gly Lys Ser Thr Leu Leu Lys Arg Leu Phe Ala Glu
20        25        30

Tyr Pro Asp Thr Phe Asp Leu Ser Val Ser His Thr Thr Arg Ala Pro
35        40        45

Arg Pro Gly Glu Glu Asn Gly Arg Glu Tyr Tyr Phe Thr Thr Lys Glu
50        55        60

Asp Phe Leu Asp Leu Val Ser Lys Asn Ala Phe Ile Glu His Ala Gln
65        70        75        80

Phe Gly Gly Asn Tyr Tyr Gly Thr Thr Val Gln Ala Val Lys Asp Val
85        90        95

Ala Gln Lys Gly Lys Ile Cys Val Leu Asp Ile Glu Met Glu Gly Val
100       105       110

Lys Gln Val Lys Arg Thr Asp Leu Asp Ala Arg Phe Leu Phe Leu Ala
115       120       125

Pro Pro Ser Leu Glu Glu Leu Glu Lys Arg Leu Arg Gly Arg Ala Thr
130       135       140

Glu Thr Glu Glu Ser Leu Thr Lys Arg Leu Ala Gln Ala Lys Asn Glu
145       150       155       160

Leu Glu Tyr Ala Ala Gln Pro Gly Ser His Asp Lys Ile Val Val Asn
165       170       175

Asp Asp Leu Glu Lys Ala Tyr Lys Glu Leu Arg Asp Trp Ile Val Asp
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PCT/IB03/01374

Gly Gly Asn Phe Gly Ala Arg Gln
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<210> 123
<211> 3108
<212> DNA
<213> *Aspergillus fumigatus*

<220>
<223> Phylum CEA255; clone 10-3-7; contig 4899 region 441274-438167
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 123
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acacaagaag tgcttacaac atgttagaag ccttcgaagt cttgacaaca tctggggttg 540
tgctgtggtc gaagtgcgtat gcgccggtcg gagcgcatgt tgtcaacagc ctaatcaacg 600
atgtcttcat tgaggagaag gttcgagcgc agaatcaggc agcgagcagt gcagtcctta 660
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<210> 124

<211> 2059

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA255; clone 10-3-7; contig 4899 region 441274-438167
 Genomic sequence containing the coding region

<400> 124

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<210> 125

<211> 1884

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA255; clone 10-3-7; contig 4899 region 441274-438167

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PCT/IB03/01374

Coding region without introns

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<210> 126

<211> 641

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA255; clone 10-3-7; contig 4899 region 441274-438167
Protein sequence

<400> 126

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Asn Asp Val Phe Ile Glu Glu Lys Val Arg Ala Gln Asn Gln Ala Ala
35          40          45

Ser Ser Ala Ala Pro Ile Tyr Lys Lys Glu Lys Tyr Thr Leu Lys Trp
50          55          60

Lys Gln Val Lys Asp Phe Asn Leu Ile Phe Val Ala Val Tyr Gln Ser

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PCT/IB03/01374

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Ile Ile Glu Tyr Pro Phe Asp Lys Tyr Phe Asp Gln Gln Val Arg Glu	115	120	125
Leu Glu Asp Asn Ala Gly Ala Pro Thr Ser Glu Ser Leu Val Val Glu	130	135	140
Ile Asn Glu Arg Lys Asp Pro Leu Val Ser Ser Asp Asn Gly Gly Pro	145	150	155
Pro Pro Pro Pro Val Pro Val Ala Gln Gly Val Ala Thr Ser Asp Glu	165	170	175
Gly Ser Pro Pro Gln Thr Pro Asp Leu Ser Arg Ser Ser Thr Pro Ile	180	185	190
Ser Gly His Leu Leu Thr Ala Lys Gly Gly Pro Ala Gly Arg Ala Ser	195	200	205
Arg Arg Ala Arg Lys Ala Ala Asn Ala Ser Ala Thr Ala Ser Ser Gly	210	215	220
Asp Glu Ser Ile Arg Lys Gly Lys Thr Leu Lys Ser Gly Lys Lys Met	225	230	235
Arg Lys Trp Asp Ala Asp Gly Phe Ala Asp Glu Asp Asp Gly Lys Val	245	250	255
Leu Asp Tyr Ser Ala Pro Ala Asp Gly Glu Asp Ala Pro Ala Pro Val	260	265	270
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Gln Phe Val Leu Lys Asp Leu Gly Asp Glu Val His Ser Ile Leu Glu	290	295	300
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Gly Lys Val Leu Thr Glu Ala Asp Leu Glu Lys Pro Leu Lys Ala Met	340	345	350
Glu Asp His Leu Leu Lys Lys Asn Val Ala Arg Glu Ala Ala Val Arg	355	360	365
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Phe Gln Ser Val Asp Ala Ala Leu Arg Ser Ala Met Glu Ser Ser Leu	385	390	395
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PCT/IB03/01374

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 Ala Ala Cys Asp Thr Phe Arg Ser Gly Ala Val Glu Gln Leu Arg Val
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 His Ala Arg Asn Leu Lys Glu Leu Ser Thr Arg Glu Asn Ala Gly Glu
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 Val Glu Leu Tyr Glu Lys Gly Tyr Gly Lys Asp Ala Ala Asn Val Ala
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 Lys Asp Ala Val Glu Tyr Gly Ala Ala Asn His Phe Asp Val Val Leu
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 Lys Cys Asp Thr Val Gly Asp Met Val Gly Thr Leu Val Ser Met Val
 595 600 605
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<210> 127

<211> 2564

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA256; clone 2-6-4; contig 4938 region 582107-579544
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 127

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WO 03/076464

PCT/IB03/01374

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<210> 128

<211> 1564

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA256; clone 2-6-4; contig 4938 region 582107-579544
Genomic sequence containing the coding region

<400> 128

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PCT/IB03/01374

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<210> 129

<211> 1383

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA256; clone 2-6-4; contig 4938 region 582107-579544
Coding region without introns

<400> 129

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<210> 130

<211> 460

<212> PRT

WO 03/076464

PCT/IB03/01374

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA256; clone 2-6-4; contig 4938 region 582107-579544
Protein sequence

<400> 130

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Ala Thr Glu Lys Glu Leu Tyr Ser Lys Leu Trp Ala Asp Leu Glu Gly
35          40          45

Tyr Asn Leu Asp Phe Glu Ser Pro Lys Asn Asp Lys Leu Ser Leu Phe
50          55          60

Glu Leu Gly Asp Arg Val Tyr Asp His Met Leu Leu Leu Pro Pro Lys
65          70          75          80

Ser Lys Gly Tyr Gly Pro Ser Leu Thr Pro Lys Asn Ile Ile Asp Phe
85          90          95

Met Asn Lys Asp Gly Asn Val Leu Leu Ala Leu Ser Gly Lys Ser Thr
100         105         110

Thr Ala Ser Ala Ile Ser Ser Leu Leu Leu Glu Leu Asp Leu His Leu
115         120         125

Pro Val Asp Arg Ser Ser Val Thr Val Asp His Phe Asn Tyr Asp Thr
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Leu Ser Ala Ser Asp Lys His Asp Val Leu Leu Leu His Arg Pro Gly
145         150         155         160

Lys Leu Arg Ser Asp Thr Lys Ala Phe Phe Asp Gly Glu Gly Val Val
165         170         175

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180         185         190

Ile Ala Pro Ile Leu Arg Ala Pro Ala Thr Ala Tyr Ser Tyr Asn Pro
195         200         205

Lys Glu Asp Ala Ser Ser Val Glu Asp Val Ala Ala Thr Gly Ser Gln
210         215         220

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245         250         255

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260         265         270

Phe Ala Lys Gln Leu Thr Ala Trp Thr Phe Lys Glu Thr Gly Val Leu
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PCT/IB03/01374

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 305 310 315 320

Phe Ser Ile Glu Leu Ser Glu Tyr Asn Tyr Asp Arg Tyr Ala Pro Phe
 325 330 335

Glu Val Pro Thr Gly Asp Ala Val Gln Leu Glu Phe Thr Met Leu Ser
 340 345 350

Pro Phe His Arg Leu Asn Leu Glu Pro Val Arg Arg Thr Asp Asn Ser
 355 360 365

Thr Val Tyr Ser Thr Arg Phe Thr Thr Pro Asp Gln His Gly Ile Phe
 370 375 380

Ser Phe Arg Val Asn Tyr Lys Arg Pro Phe Leu Thr Asn Ile Glu Glu
 385 390 395 400

Lys Leu Glu Val Thr Val Arg His Phe Ala His Asn Glu Tyr Pro Arg
 405 410 415

Ser Trp Lys Ile Ser Gly Gly Trp Val Trp Ile Ala Gly Leu Trp Ser
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Val Ile Ala Gly Phe Leu Val Phe Val Val Ala Trp Leu Tyr Ser Ala
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<210> 131

<211> 3376

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA257; clone 2-1-1; contig 4951 region 8362-11737
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 131

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PCT/IB03/01374

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<210> 132

<211> 2376

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA257; clone 2-1-1; contig 4951 region 8362-11737
Genomic sequence containing the coding region

<400> 132

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PCT/IB03/01374

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<210> 133

<211> 2148

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA257; clone 2-1-1; contig 4951 region 8362-11737

Coding region without introns

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PCT/IB03/01374

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<210> 134

<211> 715

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA257; clone 2-1-1; contig 4951 region 8362-11737
Protein sequence

<400> 134

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Ser Pro Val Ile Ser Ile Thr Tyr Glu Asp Thr Ala Val Leu Arg Glu
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Gly Asp Lys Ala Val Val Gln Tyr Thr Gly Ala Ser Gly Asn Pro Ile
50          55          60

Phe Gly Leu Ile Asn Ala Val Gln Glu Leu Arg Lys Asp Phe Pro Phe
65          70          75          80

Leu Asn Ser Lys Asp Glu Lys Leu Glu Asn Glu Trp Leu Ser Gln Leu
85          90          95

Glu Ala Phe Ala Pro Leu Asp Phe Lys Ala Leu Asp Pro Glu Leu Gln
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Arg Leu Asp Thr His Leu Leu Leu Arg Ser Phe Val Val Gly Tyr Ala
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Leu Ser Thr Ala Asp Ile Ala Leu Trp Gly Ala Ile Arg Gly Asn Arg
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Val Ala Val Ala Ala Ile Lys Lys Gly Ser Leu Val Asn Val Thr Arg

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WO 03/076464

PCT/IB03/01374

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Glu Val Leu Asn Gln Ala Val Arg Glu Lys Lys Ala Ala Lys Ala Lys						
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Glu Gly Ala Ser Tyr Asp Ile Ala Leu Leu Asn Thr Glu Lys Gly Val						
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Ala Lys Ala Ala Leu Leu Asn Asp Tyr Phe Ala His Glu Lys Tyr Asn						
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Gly Thr Leu Leu Val Arg Phe Asp Asp Thr Asn Pro Ser Asn Glu Lys						
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Val Thr His Ala Leu Arg Thr Ile Glu Tyr Arg Asp Arg Asn Pro Gln						
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Tyr Gln Trp Phe Leu Asp Thr Leu Lys Leu Arg His Val Gln Ile Trp						
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Asp Phe Ala Arg Met Asn Phe Ile Arg Thr Leu Leu Ser Lys Arg Lys						
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Leu Thr Lys Leu Val Asn Gln Gly Val Val Trp Gly Trp Asp Asp Pro						
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PCT/IB03/01374

Ala Leu Arg Glu Phe Ile Leu Lys Gln Gly Pro Ser Lys Asn Ile Thr
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Asn Leu Asp Trp Thr Leu Ile Trp Ala Thr Asn Lys Lys Tyr Ile Asp
500 505 510

Pro Val Ala Pro Arg His Thr Ala Ile Leu Lys Lys Asp Met Val Lys
515 520 525

Ala Ile Val Lys Gly Gly Pro Ala Thr Pro Tyr Thr Glu Glu Lys Pro
530 535 540

Lys His Gly Lys Asn Pro Ala Val Gly Met Lys Lys Val Val Phe Gly
545 550 555 560

Asn Thr Val Ile Phe Asp Gln Lys Asp Ala Lys Ser Phe Lys Gln Asp
565 570 575

Glu Glu Ile Thr Leu Met Ser Trp Gly Asn Ala Ile Val Arg Lys Ile
580 585 590

Glu Thr Asp Pro Thr Ser Gly Ile Val Lys Glu Leu Glu Leu Glu Leu
595 600 605

His Leu Glu Gly Asp Phe Lys Lys Thr Glu Lys Lys Val Thr Trp Leu
610 615 620

Ser Thr Glu Gly Gln Asp Leu Ile Pro Val Glu Leu Val Asp Phe Asp
625 630 635 640

Tyr Leu Leu Asn Lys Asp Thr Leu Gln Glu Asp Asp Val Leu Glu Asp
645 650 655

Val Leu Asn Lys Asn Thr Glu Phe Arg Glu Asp Ala Val Ala Asp Cys
660 665 670

Asn Val Ala Glu Leu Lys Glu Gly Asp Ile Ile Gln Phe Glu Arg Lys
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<210> 135

<211> 3639

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA258; clone 2-10-16; contig 4912 region 46084-42446
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 135

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PCT/IB03/01374

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<210> 136

<211> 2639

WO 03/076464

PCT/IB03/01374

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA258; clone 2-10-16; contig 4912 region 46084-42446
Genomic sequence containing the coding region

<400> 136

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<210> 137

<211> 2430

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA258; clone 2-10-16; contig 4912 region 46084-42446

WO 03/076464

PCT/IB03/01374

Coding region without introns

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<210> 138

<211> 809

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA258; clone 2-10-16; contig 4912 region 46084-42446
Protein sequence

<400> 138

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WO 03/076464

PCT/IB03/01374

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 Arg Thr Ile Gln Ala Ile Ser Gly Glu Tyr Pro Met Asp Pro Pro Pro
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 Pro Glu Asp Gln Ile Ser Ala Gln Ile Asp Arg Glu Ala Thr Asn Ala
 340 345 350

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Pro Arg Val Gly Asp Arg Lys Arg Thr Val Ser Gly Gln Val Ala His
 355 360 365
 Pro Pro Thr Ser Gln Pro Thr Glu Pro Gly Ala Pro Gln Arg Arg Ser
 370 375 380
 Val Arg Leu Phe Asn Gln Ile Lys Pro Thr Thr Ser Lys Leu Ser Ala
 385 390 395 400
 Ser Ala Leu Gly Val Lys Asp Ala Arg Glu Val Lys Lys Ala Lys Ala
 405 410 415
 Thr Gly Thr Lys Gly Arg Thr Thr Thr Thr Thr Met Gly Arg Val Val
 420 425 430
 Ser Gly Ser Arg Lys His Ala Ser Glu His His Asp Ala Asp Gly Lys
 435 440 445
 Asp Gly Arg Ser Val Pro Ser Ala His Thr His Ala Ile Ser Lys Gly
 450 455 460
 Ala Ala Gln Glu Arg Ser Lys Glu Ile Glu Ala Leu Thr Trp Leu Leu
 465 470 475 480
 Glu Leu Phe Ser Lys Leu Ala Ser Gly Phe Phe Ala Leu Cys Arg Tyr
 485 490 495
 Arg Cys Pro Glu Ser Ile Gln Ile Phe Asn Ser Leu Ser Gln Gly Gln
 500 505 510
 Arg Glu Thr Pro Trp Val Leu Ala Gln Ile Gly Arg Ala Tyr Tyr Glu
 515 520 525
 Gln Ala Met Tyr Ser Glu Ala Glu Lys Tyr Phe Tyr Arg Val Lys Thr
 530 535 540
 Met Ala Pro Ser Arg Leu Glu Asp Met Glu Ile Tyr Ser Thr Val Leu
 545 550 555 560
 Trp His Leu Lys Asn Asp Val Glu Leu Ala Tyr Leu Ala His Glu Leu
 565 570 575
 Met Glu Thr Asp Arg Leu Ser Pro Gln Ala Trp Cys Ala Ile Gly Asn
 580 585 590
 Ser Phe Ser His Gln Arg Asp His Asp Gln Ala Leu Lys Cys Phe Lys
 595 600 605
 Arg Ala Thr Gln Leu Asp Pro Gln Phe Ala Tyr Gly Phe Thr Leu Gln
 610 615 620
 Gly His Glu Tyr Val Ala Asn Glu Glu Tyr Asp Lys Ala Leu Asp Ala
 625 630 635 640
 Tyr Arg His Gly Ile Ser Ala Asp Ser Arg His Tyr Asn Ala Trp Tyr
 645 650 655
 Gly Leu Gly Thr Val Tyr Asp Lys Met Gly Lys Leu Asp Phe Ala Glu
 660 665 670
 Gln His Phe Arg Asn Ala Ala Ser Ile Asn Pro Thr Asn Ala Val Leu

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675	680	685
Ile Cys Cys Ile Gly Leu Val Leu Glu Lys Met Asn Asn Pro Lys Ala		
690	695	700
Ala Leu Val Gln Tyr Gly Arg Ala Cys Ser Leu Ala Pro His Ser Val		
705	710	715
Leu Ala Arg Phe Arg Lys Ala Arg Ala Leu Met Lys Leu Gln Glu Leu		
	725	730
Lys Leu Ala Leu Ser Glu Leu Lys Ile Leu Lys Asp Met Ala Pro Asp		
	740	745
Glu Ala Asn Val His Tyr Leu Leu Gly Lys Leu Tyr Lys Met Leu His		
	755	760
Asp Lys Ala Asn Ala Ile Lys His Phe Thr Thr Ala Leu Asn Leu Asp		
	770	775
Pro Lys Ala Ala Gln Tyr Ile Lys Asp Ala Met Glu Ser Leu Asp Asp		
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Asp Glu Glu Asp Asp Glu Asp Met Ser		
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<210> 139

<211> 2684

<212> DNA

<213> Aspergillus fumigatus

<220>

<223> Phylum CEA259; clone 5-4-21; contig 4963 region 373462-376145
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 139

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acattccacc	ggctcaatgg	ggtcgaatgg	tcacacaagg	atgtccgaaa	attgggaagg	120
aagagatcaa	agacaagtcc	caatgtccac	gcgtgaggta	gcaacgcccg	ggaacagacc	180
tggtcctttt	gcgaccttgc	acgatcgagg	gaaggtggct	aagcaaccog	atttctatga	240
tccttacttt	ccgctcaaat	atctggagggt	accgaaatgt	acgtgagccc	tgccgtcaaa	300
ttactaccgc	ctgcttactt	gtcatggcct	ataactgacc	ctgccctgca	gccgatcata	360
tttataaaaag	agcccactac	ggtttacaat	cggttaattcc	cgatgagggtg	gactttgcat	420
tgtatcacct	tggttcagatt	tcgaatcaac	gatgggataa	attcaagttt	gaggggtttcc	480
ccttgcttgc	ggagaacctc	atggcaaagg	ccctggatat	ctcccttgtc	acaaccgggg	540
tgaagtggga	gcttcagtat	gatgttcttc	aactcagtga	tcgcgtcaat	gagctgaact	600
cgctacatgg	cacacgagat	ctgttgagga	agatcaaaca	aatgccagtt	acattgccgg	660
aagacaccct	cgagacgtac	gaattcaacc	accttctgcg	caacgttaaa	gaagcgaccc	720
tggtactacg	caatatggtc	cttctgaaaag	agaatgccta	ctatgtgtca	cggtacgcga	780
aaggcctgct	ccgagacttc	ctcgtcatta	tgatcaactt	gcccaatcag	cctcgtctca	840
acgagatcaa	gaacgacgct	ttggacattg	cagaggagggt	caccaagttt	atgaagaccg	900
atccggaaga	tccacttttg	atctcacttc	tcaattgtct	cgggtcgtca	gatcgtgctc	960
acgtgggtccg	cgcaactctg	gctctcacc	atttctccac	tgaattagac	gagccagagg	1020
cgaaccgggc	aatggaacgg	ataccaaaaag	agactttgca	gcagctctac	tttcacactc	1080
ttctcgactt	ggacaaagat	attctcagtg	gtgcattgga	cttctggtac	cagtatacac	1140
tttcgtccga	gaacattgag	actttgattg	aggtcttcaa	cttgccctacc	gtcttcgtcc	1200
cccggatggt	cgcactgtta	acgcacgaag	gccgaccgaa	caagaaggaa	actgtgttgc	1260
aagaagaaaa	ggtggccccc	ccaccgtcgg	atatccctcg	tgtaccgccc	gagctcatga	1320
aagagctgat	ggagctttcg	gagcctgaac	ggagctcgcg	ttggctccgg	tgctgctttg	1380
tggaggacct	cgagtgcgag	atcacccaaa	ttgccttgtg	gcaggcgtat	cagagcagat	1440

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tcagtacgac	tttcacgaac	gcgcaagcac	aggtgatcaa	tggccctggt	gcagccacga	1560
aattcatcat	caaaggcatt	cggccctggt	agaccgccta	taccttcgag	ggctttccct	1620
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aaacgcggcg	acactataac	ctggagaagg	cggagtcgcc	cgttcatacc	tgcctttggg	1800
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aacttaccga	gttgatcatg	gtaatagaaa	aagaggatta	ttactgaact	tggggcgcgga	2220
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agaaaagata	ctaatacgct	aggtgctcaa	tgattccagg	tcacttggaa	aattgatcgg	2640
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<210> 140

<211> 1707

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA259; clone 5-4-21; contig 4963 region 373462-376145
Genomic sequence containing the coding region

<400> 140

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gaattcaacc	accttctg	caacgttaaa	gaagcgaccc	tggtagtacg	caatatggtc	240
cttctgaaa	agaatgccta	ctatgtgtca	cggtagcgga	aaggcctgct	ccgagacttc	300
ctcgtcatta	tgatcaactt	gcccacacag	cctcgtctca	acgagatcaa	gaacgacgct	360
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gcacgcgagt	acaacgggct	ttcatggaag	aaagccgtct	tccttagtca	tcgtccaaag	1620
atcatcgaa	catgggaccg	caaccgctca	ttgcgcaagg	aacttaccga	gttgatcatg	1680

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gtaatagaaa aagaggatta ttactga

1707

<210> 141

<211> 1707

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA259; clone 5-4-21; contig 4963 region 373462-376145
Coding region without introns

<400> 141

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ctgttgagaga	agatcaaaca	aatgccagtt	acattgccgg	aagacaccct	cgagacgtac	180
gaattcaacc	accttctgcg	caacgttaaa	gaagcgaccc	tggtactacg	caatatggtc	240
cttctgaaag	agaatgccta	ctatgtgtca	cggtagcgga	aaggcctgct	ccgagacttc	300
ctcgtcatta	tgatcaactt	gcccatacag	cctcgtctca	acgagatcaa	gaacgacgct	360
ttggacattg	cagaggagggt	caccaagttt	atgaagaccg	atccggaaga	tccactttgg	420
atctcacttc	tcaattgtct	cggtctgtca	gatcgtgctc	acgtggtccg	cgactctgg	480
gctctcacc	atttctccac	tgaattagac	gagccagagg	cgaaccgggc	aatggaacgg	540
ataccaaaag	agactttgca	gcagctctac	tttcacactc	ttctcgactt	ggacaaagat	600
attctcagtg	gtgcattgga	cttctgttac	cagtatacac	tttcgtccga	gaacattgag	660
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ggtggcggtg	ttctccctgc	ggctgaattt	atcaaaaatg	tcagtacgac	tttcacgaac	1020
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ctggagaagg	cggagtcgcc	cgttcatacc	tgcctttggg	acaactgcac	gaaattccgg	1320
tcgtctggtc	cgagtgccta	tactgcaatg	gtcgtgtggc	acgtctccgc	acatctgccc	1380
gaggaacgtg	cgccagatgc	ggagccgccc	acatccaaac	gtgcggttct	ccaagagcgc	1440
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gtggcctaca	aggcggcggt	agtattgcgt	aaccttgccc	gaaacctgcc	tacgggtatt	1560
gcaccgcagt	acaacgggct	ttcatggaag	aaagccgtct	tccttagtca	tcgtccaaag	1620
atcatcgaag	catgggaccg	caaccgctca	ttgcgcgaag	aacttaccga	gttgatcatg	1680
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<210> 142

<211> 568

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA259; clone 5-4-21; contig 4963 region 373462-376145
Protein sequence

<400> 142

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Glu	Leu	Gln	Tyr	Asp	Val	Leu	Gln	Leu	Ser	Asp	Arg	Val	Asn	Glu	Leu
			20					25					30		

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Asn Ser Leu His Gly Thr Arg Asp Leu Leu Glu Lys Ile Lys Gln Met
  35                               40                               45

Pro Val Thr Leu Pro Glu Asp Thr Leu Glu Thr Tyr Glu Phe Asn His
  50                               55                               60

Leu Leu Arg Asn Val Lys Glu Ala Thr Leu Val Leu Arg Asn Met Val
  65                               70                               75                               80

Leu Leu Lys Glu Asn Ala Tyr Tyr Val Ser Arg Tyr Ala Lys Gly Leu
                               85                               90                               95

Leu Arg Asp Phe Leu Val Ile Met Ile Asn Leu Pro Asn Gln Pro Arg
  100                               105                               110

Leu Asn Glu Ile Lys Asn Asp Ala Leu Asp Ile Ala Glu Glu Val Thr
  115                               120                               125

Lys Phe Met Lys Thr Asp Pro Glu Asp Pro Leu Trp Ile Ser Leu Leu
  130                               135                               140

Asn Cys Leu Gly Ser Ser Asp Arg Ala His Val Val Arg Ala Leu Trp
  145                               150                               155                               160

Ala Leu Thr His Phe Ser Thr Glu Leu Asp Glu Pro Glu Ala Asn Arg
                               165                               170                               175

Ala Met Glu Arg Ile Pro Lys Glu Thr Leu Gln Gln Leu Tyr Phe His
  180                               185                               190

Thr Leu Leu Asp Leu Asp Lys Asp Ile Leu Ser Gly Ala Leu Asp Phe
  195                               200                               205

Trp Tyr Gln Tyr Thr Leu Ser Ser Glu Asn Ile Glu Thr Leu Ile Glu
  210                               215                               220

Val Phe Asn Leu Pro Thr Val Phe Val Pro Arg Met Val Ala Leu Leu
  225                               230                               235                               240

Thr His Glu Gly Arg Pro Asn Lys Lys Glu Thr Val Leu Gln Glu Glu
                               245                               250                               255

Lys Val Ala Pro Pro Pro Ser Asp Ile Pro Arg Val Pro Pro Glu Leu
  260                               265                               270

Met Lys Glu Leu Met Glu Leu Ser Glu Pro Glu Arg Ser Ser Arg Trp
  275                               280                               285

Leu Arg Cys Cys Phe Val Glu Asp Leu Glu Cys Glu Ile Thr Gln Ile
  290                               295                               300

Ala Leu Trp Gln Ala Tyr Gln Ser Arg Phe Ala Asp Pro Arg Leu Pro
  305                               310                               315                               320

Gly Gly Gly Val Leu Pro Ala Ala Glu Phe Ile Lys Asn Val Ser Thr
  325                               330                               335

Thr Phe Thr Asn Ala Gln Ala Gln Val Ile Asn Gly Pro Gly Ala Ala
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Thr Lys Phe Ile Ile Lys Gly Ile Arg Pro Leu Glu Thr Ala Tyr Thr
355 360 365

Phe Glu Gly Phe Pro Tyr Ile Tyr Cys Lys Trp Ala Asp Asn Ser Lys
370 375 380

Pro Ser Lys Thr Cys Gln Arg Ala Phe Lys Ser Pro Ala Glu Leu Arg
385 390 395 400

His His Val Phe Thr Glu His Met Asn Leu Lys Pro Thr Glu Thr Pro
405 410 415

Gly His Tyr Asn Leu Glu Lys Ala Glu Ser Pro Val His Thr Cys Leu
420 425 430

Trp Asp Asn Cys Thr Lys Phe Arg Ser Ser Gly Pro Ser Ala Asn Thr
435 440 445

Ala Met Val Ala Gly His Val Ser Ala His Leu Pro Glu Glu Arg Ala
450 455 460

Pro Asp Ala Glu Pro Pro Thr Ser Lys Arg Ala Val Leu Gln Glu Arg
465 470 475 480

Ile Val Arg Lys Trp Tyr Tyr Leu Asp Thr Pro Val Asn Glu Arg Gly
485 490 495

Glu Pro Phe Gly Val Ala Tyr Lys Ala Ala Leu Val Leu Arg Asn Leu
500 505 510

Ala Arg Asn Leu Pro Thr Gly Ile Ala Pro Gln Tyr Asn Gly Leu Ser
515 520 525

Trp Lys Lys Ala Val Phe Leu Ser His Arg Pro Lys Ile Ile Glu Ala
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Trp Asp Arg Asn Arg Ser Leu Arg Lys Glu Leu Thr Glu Leu Ile Met
545 550 555 560

Val Ile Glu Lys Glu Asp Tyr Tyr
565

<210> 143

<211> 2542

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA260; clone 2-10-21; contig 4849 region 12560-15101
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 143

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aaaagcagat  actctcgtct  gctagaccgc  atactttgac  cggatcgggt  atcttccagt     180
acgagggtgc  tcggcatata  gtcacaattc  ctttttcaag  aggctttttc  ctctctcccc     240
tattcctttc  cctccctag  catcccttcc  gagcttgcc  taatttcgtc  catctggcct     300
gtgtgccatt  ctcttcattg  cgatcaaggg  ccttctctct  caggcggaca  cagccccct      360
gttcgtctgg  gcagcagata  gtgcttccta  ggcttctgtg  tctacgggta  actacatata     420
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PCT/IB03/01374

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gactcgtagt agaatgtgtt gatccagttg atggccgacg ccaactggta tcgattacgg 2460
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caacacgaca ttcaactttc aa 2542

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<210> 144

<211> 1542

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA260; clone 2-10-21; contig 4849 region 12560-15101
Genomic sequence containing the coding region

<400> 144

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atggtctaca tcggcatccc caagaactac acggcttcgc cgtcttcctt tgccggaact 60
ccgtccttga cgatcaatta cgaggcaacg caggatcttg attctaccaa tgcttttgaa 120
ggtttgttga cgccggtgac acgtgtgaga gcagcgctgg acagaggctg acagtctaca 180
ggtccagaga aactcttgga ggtgtggttc gcgccttccg ctcaggaatt aggtccagcg 240
cagcccgccg gtctgaaggc tgttccggag gagatctgga aggacatgtt ggatctcgtc 300
aattgccagg tcctctcgat tgtttcgtca gaggatgtgg acgcctacct gctctccgag 360
tctagcatgt tcgtttgccc tcacaaactc atcttgaaga cttgtggtac caccactctt 420
ctgtctggtc tcccacgcat tctcgagatt gccgctttgt tcggtggctt ccccaagtct 480
accgcccctt ctgcgcgaat ctccgtcgcc gctgcgccct acccgctctt ctacagccgc 540
aagaacttcc tgttccccga ccgccagcgg ggccctcacc gcagctggag agatgaagtg 600
cggactatgg ataagctctt cctcaacggc agcgccctaca tgattggcaa gatgaatggc 660
gagcactggg acttgtacct gactgaacct cataccatgc tcaccccgcc aacgagcccg 720
ggaaacgaga ccgagtttac ggaaacggag accaaggtcc tcagtgtacc ccagggcgct 780
gctctgcaga ctgattcgga ggatgagact ttggaagtct tgatgaccga cttggatgag 840

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WO 03/076464

PCT/IB03/01374

```

gagaacgcca agcagttcta cctcgagaat gccactgccg ttgaggagaa ccgttatcgc      900
aactcaaatt cggagaagag tggccatgtt gatgttttca gcaacacttc ctccgatatc      960
agcgattttg actccgacgg aagccagggt ctgcctccag agttgactac cgagggtcac      1020
gcgctcggaa ccgtggtctc tgaagcctgt ggactttcct ctgtgtatcc taaggagaag      1080
tatcccgatt cgcgcacatga tgcctacctg tttacaccat gcgggttctc cgccaacggc      1140
gtgattccgc ctccctgaggg aaaagctgga acccaactact tcacagtaca cgtcactcca      1200
gagccgcact gttcatatgc gtcccttgag accaacgtac cgcactcgca gaacggccag      1260
actaccgctg gaatcatcaa gcaagtggtc gacatcttca agcctggtcg cttcagcgtg      1320
actctcttcg aggccaagcc agcgtctgag caggctgaag acgagtggaa ggaagccaag      1380
tacctggccg ctctctcgac cgccaaaatg gaacatgtgg agggatatcg ccgagtggac      1440
cggattgtcc acgacctcga cggctatgag cttgtcttcc gctattatga acgcctggac      1500
tggaaggagg gggccctcgc gctgggagag gagagatctt ga      1542

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<210> 145
 <211> 1482
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA260; clone 2-10-21; contig 4849 region 12560-15101
 Coding region without introns

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<400> 145
atggtctaca tcggcatccc caagaactac acggcttcgc cgtcttccct tgccggaact      60
ccgtccettga cgatcaatta cgaggcaacg caggatcttg attctaccaa tgcttttgaa      120
ggtccagaga aactcttgga ggtgtggttc gcgccttcgc ctccaggaatt aggtccagcg      180
cagcccgccg gtctgaaggc tgttcgagag gagatctgga aggacatgtt ggtctcgtc      240
aattgccagg tcctctcgat tgtttcgtca gaggatgtgg acgcctacct gctctccgag      300
tctagcatgt tcgtttggcc tcacaaaact atcttgaaga cttgtggtac caccactctt      360
ctgtctggtc tcccacgcat tctcgagatt gccgctttgt tcggtggctt cccaagtct      420
accgcccctt ctgcggaat ctccgtcgcc gctgcgccct accgcgtctt ctacagccgc      480
aagaacttec tgttcccga cgcgcagcgg ggccctcacc gcagctggag agatgaagtg      540
cggactatgg ataagctctt cctcaacggc agcgcctaca tgattggcaa gatgaatggc      600
gagcactggt acttgtaact gactgaacct cataccatgc tcaccccgcc aacgagcccg      660
ggagccaaga ccgagtttac ggaaacggag accaaggtcc tcagtgtacc ccagggcgct      720
gctctgcaga ctgattcgga ggatgagact ttggaagtct tgatgaccga cttggatgag      780
gagaacgcca agcagttcta cctcgagaat gccactgccg ttgaggagaa ccgttatcgc      840
aactcaaatt cggagaagag tggccatgtt gatgttttca gcaacacttc ctccgatatc      900
agcgattttg actccgacgg aagccagggt ctgcctccag agttgactac cgagggtcac      960
gcgctcggaa ccgtggtctc tgaagcctgt ggactttcct ctgtgtatcc taaggagaag      1020
tatcccgatt cgcgcacatga tgcctacctg tttacaccat gcgggttctc cgccaacggc      1080
gtgattccgc ctccctgaggg aaaagctgga acccaactact tcacagtaca cgtcactcca      1140
gagccgcact gttcatatgc gtcccttgag accaacgtac cgcactcgca gaacggccag      1200
actaccgctg gaatcatcaa gcaagtggtc gacatcttca agcctggtcg cttcagcgtg      1260
actctcttcg aggccaagcc agcgtctgag caggctgaag acgagtggaa ggaagccaag      1320
tacctggccg ctctctcgac cgccaaaatg gaacatgtgg agggatatcg ccgagtggac      1380
cggattgtcc acgacctcga cggctatgag cttgtcttcc gctattatga acgcctggac      1440
tggaaggagg gggccctcgc gctgggagag gagagatctt ga      1482

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<210> 146
 <211> 493
 <212> PRT
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA260; clone 2-10-21; contig 4849 region 12560-15101
 Protein sequence

<400> 146

WO 03/076464

PCT/IB03/01374

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Met Val Tyr Ile Gly Ile Pro Lys Asn Tyr Thr Ala Ser Pro Ser Ser
1      5      10      15

Phe Ala Gly Thr Pro Ser Leu Thr Ile Asn Tyr Glu Ala Thr Gln Asp
20      25      30

Leu Asp Ser Thr Asn Ala Phe Glu Gly Pro Glu Lys Leu Leu Glu Val
35      40      45

Trp Phe Ala Pro Ser Ala Gln Glu Leu Gly Pro Ala Gln Pro Ala Gly
50      55      60

Leu Lys Ala Val Pro Glu Glu Ile Trp Lys Asp Met Leu Asp Leu Val
65      70      75      80

Asn Cys Gln Val Leu Ser Ile Val Ser Ser Glu Asp Val Asp Ala Tyr
85      90      95

Leu Leu Ser Glu Ser Ser Met Phe Val Trp Pro His Lys Leu Ile Leu
100     105     110

Lys Thr Cys Gly Thr Thr Thr Leu Leu Ser Gly Leu Pro Arg Ile Leu
115     120     125

Glu Ile Ala Ala Leu Phe Gly Gly Phe Pro Lys Ser Thr Ala Pro Ser
130     135     140

Arg Gly Ile Ser Val Ala Ala Ala Pro Tyr Arg Val Phe Tyr Ser Arg
145     150     155     160

Lys Asn Phe Leu Phe Pro Asp Arg Gln Arg Gly Pro His Arg Ser Trp
165     170     175

Arg Asp Glu Val Arg Thr Met Asp Lys Leu Phe Leu Asn Gly Ser Ala
180     185     190

Tyr Met Ile Gly Lys Met Asn Gly Glu His Trp Tyr Leu Tyr Leu Thr
195     200     205

Glu Pro His Thr Met Leu Thr Pro Pro Thr Ser Pro Gly Ala Lys Thr
210     215     220

Glu Phe Thr Glu Thr Glu Thr Lys Val Leu Ser Val Pro Gln Gly Ala
225     230     235     240

Ala Leu Gln Thr Asp Ser Glu Asp Glu Thr Leu Glu Val Leu Met Thr
245     250     255

Asp Leu Asp Glu Glu Asn Ala Lys Gln Phe Tyr Leu Glu Asn Ala Thr
260     265     270

Ala Val Ala Glu Asn Arg Tyr Arg Asn Ser Asn Ser Glu Lys Ser Gly
275     280     285

His Val Asp Val Phe Ser Asn Thr Ser Ser Asp Ile Ser Asp Phe Asp
290     295     300

Ser Asp Gly Ser Gln Val Leu Pro Pro Glu Leu Thr Thr Glu Gly His
305     310     315     320

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WO 03/076464

PCT/IB03/01374

Ala Leu Gly Thr Val Val Ser Glu Ala Cys Gly Leu Ser Ser Val Tyr
 325 330

Pro Lys Glu Lys Tyr Pro Asp Ser Arg Ile Asp Ala Tyr Leu Phe Thr
 340 345 350

Pro Cys Gly Phe Ser Ala Asn Gly Val Ile Pro Pro Pro Glu Gly Lys
 355 360 365

Ala Gly Thr His Tyr Phe Thr Val His Val Thr Pro Glu Pro His Cys
 370 375 380

Ser Tyr Ala Ser Phe Glu Thr Asn Val Pro His Ser Gln Asn Gly Gln
 385 390 395 400

Thr Thr Ala Gly Ile Ile Lys Gln Val Val Asp Ile Phe Lys Pro Gly
 405 410 415

Arg Phe Ser Val Thr Leu Phe Glu Ala Lys Pro Ala Leu Ser Gln Val
 420 425 430

Glu Asp Glu Trp Lys Glu Ala Lys Tyr Leu Ala Ala Arg Arg Thr Ala
 435 440 445

Lys Met Glu His Val Glu Gly Tyr Arg Arg Val Asp Arg Ile Val His
 450 455 460

Asp Leu Asp Gly Tyr Glu Leu Val Phe Arg Tyr Tyr Glu Arg Leu Asp
 465 470 475 480

Trp Lys Gly Gly Ala Pro Arg Leu Gly Glu Glu Arg Ser
 485 490

<210> 147

<211> 1637

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA261; clone 7-5-9; contig 4857 region 164191-165827
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 147

aaagatagag	aagacgttgc	gcggaacctt	ttgaggaccc	tcagctctat	ttgagtgtct	60
gtcacgaggt	ccatatctgg	cgatacggag	ggctggctgt	acaattaggt	tactcttatt	120
tcctactgat	ctagtgatat	aaagtttga	tgcattatgt	aaattaaatc	tcgggggcaa	180
atgaacattt	cgaatatcgt	tataaaactc	acagaaagtg	ctgtcaatgg	cacaaattta	240
gcaatcaata	ctcatctgag	tatgttgttg	ataagtcgga	aaacaacctt	aataatttacc	300
tcattaggaa	aggtgcactc	cgtagttacc	tcgactcgcg	gttagtctgg	tgactaagtt	360
cttggcggtg	tgatgagggc	aagtcctatc	atgtgatcat	agttagggtt	tccacacacc	420
aggctctcca	atatagcaag	aaaatagaag	gattaggtct	cgtctccgaa	catccatccc	480
gccagcacac	aaccgccaaa	atgggtcgcg	ttagaaccac	ggtaagttac	agatgaagca	540
tcatgagtta	tcttcaaaaa	agcccaaaa	gagtatcatt	tctgacgaaa	tgggtttttc	600
ttcaatagac	agtcaagagg	tccgccaaag	tcattcatcga	gcgtactac	cccaagttga	660
cgctcgactt	tgagaccaac	aagcgtcttt	gcgatgagat	cgctatcatt	gcctccaagc	720
gccttcgcaa	caagtggggc	aatccatcac	tgagccgtac	aacagtcgga	atttgacttg	780
ctgacgaaaa	ctagattgct	ggttacacca	cccaccttat	gaagcgtatc	cagcgtggcc	840
ctgtccgcgg	tatctctttc	aagctgcagg	aggaggagcg	tgagcgcaag	gatcagtagc	900
ttcctgaggt	ttccgctctg	gatgtttccc	agaccgagtc	cggccagctc	gatgtcgatg	960
ccgacaccaa	ggaccttctc	aagtccatgg	gcgtaagttc	tgttctcaac	gcggttggtc	1020

WO 03/076464

PCT/IB03/01374

```

gtgggttttaa agcagtcctgt taacttatat tgcccactac agttcgacaa tctcaaggtc 1080
aacgtttgtca acgtctccca acatcaggtt caggagcgcc cccgccgctt ccggtagatg 1140
cgcgcacccc tcgagcctcg aaaaaaaagt taccgattgt cttcggtcga tctatggcgt 1200
gctcaatcac acttgctctg gctgacttcg cagctatgat gtagcctaga gacacaggaa 1260
tgaacataat tctctctgag aaagggtgtcg ctgattctcc tgggtggagat gacgcttgat 1320
tgccaaaaatt tctccttttg cttactgtcc gtttcagctc gggcgctgcg tagaaggttc 1380
tctctgcatg atgcgagga tgtcatcaga gagtcgaaac ctttggtgcg aactgcacca 1440
tcaactgcac cgcattggat cagatccata ttaatcagtc tatctacaga agtaaattgg 1500
gtatcgctcat aagcacaag acgccgtaga accacaaatc gaaccacccc atcgaattct 1560
gtcgtgacca ggctcacgcc aaaccgcgtg agattgaagc atatcatgat cagatttcct 1620
ttggcacgta gccttca

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<210> 148

<211> 637

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA261; clone 7-5-9; contig 4857 region 164191-165827
Genomic sequence containing the coding region

<400> 148

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atgggtcgcg ttagaaccaa ggtaagttac agatgaagca tcatgagtta tcttcaaaaa 60
agccccaaaa gagtatcatt tctgacgaaa tgggtttttc ttcaatagac agtcaagagg 120
tccgccaaagg tcatcatcga gcgctactac cccaagttga cgctcgactt tgagaccaac 180
aagcgtcttt gcgatgagat cgctatcatt gcctccaagc gccttcgcaa caagggtgggc 240
aatccatcac tgagccgtac aacagtcgga atttgacttg ctgacgaaaa ctagattgct 300
ggttacacca cccaccttat gaagcgtatc cagcgtggcc ctgtccgcgg tatctctttc 360
aagctgcagg aggaggagcg tgagcgcaag gatcagtag ttctgaggt ttccgctctg 420
gatgtttccc agaccgagtc cggccagctc gatgtcgatg ccgacacca ggaccttctc 480
aagtcattgg gcgtaagttc tgttctcaac gcggttgttc gtgggtttta agcagtcctg 540
taacttatat tgcccactac agttcgacaa tctcaaggtc aacgttgtca acgtctccca 600
acatcagggt caggagcgcc cccgccgctt ccggtag

```

<210> 149

<211> 420

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA261; clone 7-5-9; contig 4857 region 164191-165827
Coding region without introns

<400> 149

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atgggtcgcg ttagaaccaa gacagtcaag aggtccgcca aggtcatcat cgagcgctac 60
taccccaagt tgagcctcga ctttgagacc aacaagcgtc ttgcgatga gatcgctatc 120
attgcctcca agcgcttcg caacaagatt gctggttaca ccaccacct tatgaagcgt 180
atccagcgtg gccctgtcgg cggtatctct ttcaagctgc aggaggagga gcgtgagcgc 240
aaggatcagt acgttcctga ggtttccgct ctggatgttt ccagaccga gtccggccag 300
ctcgatgtcg atgccgacac caaggacctt ctcaagtcca tgggcttcga caatctcaag 360
gtcaacggtg tcaacgtctc ccaacatcag gttcaggagc gccccgcgg cttccggtag 420

```

<210> 150

<211> 139

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA261; clone 7-5-9; contig 4857 region 164191-165827

WO 03/076464

PCT/IB03/01374

Protein sequence

<400> 150

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Met Gly Arg Val Arg Thr Lys Thr Val Lys Arg Ser Ala Lys Val Ile
 1           5           10           15
Ile Glu Arg Tyr Tyr Pro Lys Leu Thr Leu Asp Phe Glu Thr Asn Lys
          20           25           30
Arg Leu Cys Asp Glu Ile Ala Ile Ile Ala Ser Lys Arg Leu Arg Asn
          35           40           45
Lys Ile Ala Gly Tyr Thr Thr His Leu Met Lys Arg Ile Gln Arg Gly
          50           55           60
Pro Val Arg Gly Ile Ser Phe Lys Leu Gln Glu Glu Glu Arg Glu Arg
        65           70           75           80
Lys Asp Gln Tyr Val Pro Glu Val Ser Ala Leu Asp Val Ser Gln Thr
          85           90           95
Glu Ser Gly Gln Leu Asp Val Asp Ala Asp Thr Lys Asp Leu Leu Lys
          100           105           110
Ser Met Gly Phe Asp Asn Leu Lys Val Asn Val Val Asn Val Ser Gln
          115           120           125
His Gln Val Gln Glu Arg Pro Arg Arg Phe Arg
          130           135

```

<210> 151

<211> 2037

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA262; clone 10-2-18

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 151

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aaggtagtag gtgcagatat tgttgataga catttcaaaa tgtattagtt acatgattac      60
ttacttagat gtaatctttc gataatactt tctagtcttg ttgagttcag aaggccagtg      120
tgtgctgaaa atgacagcga cctatgcggt gcccggtgtag cgaagagcac tggctggaaa      180
taagaagttt attagaggag cctcatgatg cataatcatt gtaagcgcac gatgcacaat      240
aatatatccg aattttctcca gatgacacta agataataac gaaaatatca catgacgttg      300
tgggcaggta tgtattatgt aatctgatcg gtagggccga tgtctcgctt agcggacttt      360
tctgtgggat tgcaatttca acttattatt ccgccgacca gcaacaaagc ggttactcga      420
ctcgactccc tccaccagag ccggtggtgt gatataacctg tctgtctttg atcctcgcaa      480
gatagacttg agtcgcagtt atggcggttg gaaagtatgc caattcactt ctattattgt      540
tctgaacgct ttttagcatgt gtctggatac ggtggtttac aggtactgat ccgggaacag      600
gaacaagcgc ttgtcgaagg gcaagaaggg tgttaagaag aggaccgttg atcctttctc      660
caggaaggac gaataactctg ttaaggtatg tcgacgtgga ctgtgtaagt cgaccgcagc      720
taatctatat caggcgccctt ccactttcca gatcagagag tatgttgcac gcatatgatg      780
tcgaattgca ggataaaggc gattcacaaat ggtagtggag attatgctga ctgaattata      840
gtgtcgggaa gactctggtc aaccgcacca gtggtctcaa gaacgccaat gactccctga      900
agggtcgaat tttcagagtc tcgctggctg acctgcagaa tgatgaagac catgcttttc      960
gcaaggttaa gcttcgtgtg gacgaggttc agggcaagaa ctgtttgacc aacttccacg      1020
gtcttgattt cacaaccgac aaattgcgat ccctcgtcgc caagtggcag tcgctgatcg      1080
aagccaatgt cactgtgaag acgaccgatg attatctcct tcggcttttt gctatcgccct      1140

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WO 03/076464

PCT/IB03/01374

tcaccaagag	acgcccgaac	cagattaaga	agaccacata	tgctcgttct	tctcaaattcc	1200
gtgccatccg	caagaagatg	attgaaatca	tgacagaggga	ggcagccagc	tgctctctcg	1260
ctcagctcac	tcacaagctc	attcctgagg	tcattggctcg	tgagatcgag	aaggctaccc	1320
agggaatcta	tcctttgcag	aatgtgtgtg	accctgttat	tcttactcgg	gatgaagact	1380
aactgcaatc	taggtccata	ttcgcaaggt	caagcttctt	aaggctccca	agttcgacct	1440
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ggttattcgg	gacattgatt	tgtacctacc	tgtatgcttg	gattcttttt	ttatgagtta	1620
aaatgggaaa	agaacttttg	tcgcggcatc	atgtctttat	tgactgggtg	tgctcgtaa	1680
ttctatgtcc	tttgagaatg	gagcttgcaa	agaaaacttt	gcccttattc	aaatatttaa	1740
ttggacaatt	ccgatcaaa	tttagcagta	gaatacctgc	tataccagt	atgtgctgat	1800
gcaacgggca	ccgtcagttt	actttcagtt	gattcaaat	ctatattaac	agagcccttt	1860
taccacacca	ctgacctggg	attagtatag	tgtctcgccc	taggagacta	aagaattgct	1920
agaagtatgg	ttatacataa	tggtgaatag	ttagtatgat	ttattaatat	tattttcagt	1980
gcactgatat	atatcataat	gctactaaat	atagctaccc	taagatttat	atagaga	2037

<210> 152

<211> 1037

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA262; clone 10-2-18

Genomic sequence containing the coding region

<400> 152

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gtctggatac	gggtgtttac	aggtactgat	ccgggaacag	gaacaagcgc	ttgtcgaagg	120
gcaagaagg	tggttaagaag	aggaccgttg	atcctttctc	caggaaggac	gaatactctg	180
ttaaaggtag	tcgacgtgga	ctgtgttaagt	cgacgcagc	taatctatat	caggcgctt	240
ccactttcca	gatcagagag	tatgttgac	gcataatgat	tcgaattgca	ggataaaggc	300
gattcacaat	ggtagtggag	attatgctga	ctgaattata	gtgtcgggaa	gactctggtc	360
aaccgcacca	gtggtctcaa	gaacgccaat	gactccctga	agggctcgaat	tttcgaggtc	420
tcgtggctg	acctgcagaa	tgatgaagac	catgctttcc	gcaaggttaa	gcttcgtgtg	480
gacgagggtc	agggcaagaa	ctgtttgacc	aacttccacg	gtcttgattt	cacaaccgac	540
aaattgcgat	ccctcgtgcg	caagtggcag	tcgctgatcg	aagccaatgt	cactgtgaag	600
acgaccgatg	attatctcct	tcggcttttt	gctatcgctt	tcaccaagag	acgcccgaac	660
cagattaaga	agaccacata	tgctcgttct	tctcaaattcc	gtgccatccg	caagaagatg	720
attgaaatca	tgacagaggga	ggcagccagc	tgctctctcg	ctcagctcac	tcacaagctc	780
attcctgagg	tcattggctcg	tgagatcgag	aaggctaccc	agggaatcta	tcctttgcag	840
aatgtgtgtg	accctgttat	tcttactcgg	gatgaagact	aactgcaatc	taggtccata	900
ttcgcaagg	caagcttctt	aaggctccca	agttcgacct	gggtgcaactg	ctgaatctgc	960
acggtgaatc	tacaaccgat	gataagggcc	acaaggctga	gagagagttc	aaggagcagg	1020
ttctcgaaag	cgttttaa					1037

<210> 153

<211> 771

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA262; clone 10-2-18

Coding region without introns

<400> 153

atggcggttg	gaaagaacaa	gcgcttgctg	aagggaaga	aggggtgttaa	gaagaggacc	60
gttgatcctt	tctccaggaa	ggacgaatac	tctgtttaagg	cgccctccac	ttccagatc	120
agagatgtcg	ggaagactct	ggtaaccgc	accagtggtc	tcaagaacgc	caatgactcc	180
ctgaagggtc	gaattttcga	ggtctcgctg	gctgacctgc	agaatgatga	agaccatgct	240

WO 03/076464

PCT/IB03/01374

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ttccgcaagg ttaagcttcg tgtggacgag gttcagggca agaactgttt gaccaacttc 300
cacggtcttg atttcacaac cgacaaattg cgatccctcg tgcgcaagtg gcagtcgctg 360
atcgaagcca atgtcactgt gaagacgacc gatgattatc tccttcggct ttttgctatc 420
gccttcacca agagacgccc gaaccagatt aagaagacca catatgctcg ttcttctcaa 480
atccgtgcc a tccgcaagaa gatgattgaa atcatgcaga gggaggcagc cagctgctct 540
ctcgtcagc t cactcacaa gctcattcct gaggtcattg gtcgtgagat cgagaaggct 600
acccagggaa tctatccttt gcagaatgtc catattcgca aggtcaagct tcttaaggct 660
cccaagttcg acctgggtgc actgctgaat ctgcacggtg aatctacaac cgatgataag 720
ggccacaagg tcgagagaga gttcaaggag caggttctcg aaagcgttta a 771

```

<210> 154

<211> 256

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA262; clone 10-2-18

Protein sequence

<400> 154

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Met Ala Val Gly Lys Asn Lys Arg Leu Ser Lys Gly Lys Lys Gly Val
1          5          10          15

Lys Lys Arg Thr Val Asp Pro Phe Ser Arg Lys Asp Glu Tyr Ser Val
          20          25          30

Lys Ala Pro Ser Thr Phe Gln Ile Arg Asp Val Gly Lys Thr Leu Val
          35          40          45

Asn Arg Thr Ser Gly Leu Lys Asn Ala Asn Asp Ser Leu Lys Gly Arg
          50          55          60

Ile Phe Glu Val Ser Leu Ala Asp Leu Gln Asn Asp Glu Asp His Ala
65          70          75          80

Phe Arg Lys Val Lys Leu Arg Val Asp Glu Val Gln Gly Lys Asn Cys
          85          90          95

Leu Thr Asn Phe His Gly Leu Asp Phe Thr Thr Asp Lys Leu Arg Ser
          100          105          110

Leu Val Arg Lys Trp Gln Ser Leu Ile Glu Ala Asn Val Thr Val Lys
          115          120          125

Thr Thr Asp Asp Tyr Leu Leu Arg Leu Phe Ala Ile Ala Phe Thr Lys
          130          135          140

Arg Arg Pro Asn Gln Ile Lys Lys Thr Thr Tyr Ala Arg Ser Ser Gln
145          150          155          160

Ile Arg Ala Ile Arg Lys Lys Met Ile Glu Ile Met Gln Arg Glu Ala
          165          170          175

Ala Ser Cys Ser Leu Ala Gln Leu Thr His Lys Leu Ile Pro Glu Val
          180          185          190

Ile Gly Arg Glu Ile Glu Lys Ala Thr Gln Gly Ile Tyr Pro Leu Gln
195          200          205

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PCT/IB03/01374

Asn Val His Ile Arg Lys Val Lys Leu Leu Lys Ala Pro Lys Phe Asp
 210 215 220

Leu Gly Ala Leu Leu Asn Leu His Gly Glu Ser Thr Thr Asp Asp Lys
 225 230 235 240

Gly His Lys Val Glu Arg Glu Phe Lys Glu Gln Val Leu Glu Ser Val
 245 250 255

<210> 155

<211> 1819

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA263; clone 4-3-3; contig 4944 region 159432-161250
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 155

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aattcatcag cataacgaac ccccaacgac ttcgaaaaaa aagcccgatt cgaaagaatt      60
gcgcattcaa cataccatgg tggcgggcct cgtgtcgtgt cgtacgggta ttgtcgacaa      120
tgaggattga agatgggcca ggtcaatttg ggatgttcgt tgtgggacta ggggtttttt      180
ctgtgttggt gcggtcacgc tgcggctggg ctaagcgggc acgtgactgt ggctgactgc      240
ctggtgacgc ccccccccg aggaaccccc aaccggcagc cagataggct cgggaggatc      300
atcgtcgaat gatggcattg ttcttggtct cagtggatgg gttattaatg actgcctgga      360
gggctggatg actccgtcgc tgatttagca ttgtgatcca cgatttatgt ttcatttctg      420
gggcgcggtt ttactaccat cacttttgtc actaccatca cttttatact gagtttctga      480
ccccgacccc gaaccagact atggcaactt cgactgggac cggatgggct cagctccggc      540
agcaagcccc ttgcgttgag actcaggtag ggaactcgaa actacgctat aatgaggctt      600
tactcgtgat ttggatgttg acaataatgt tcctagaccg agagtctggt tcacacctat      660
gcgcagtatg catcgatgac gaagctgcct ccgaaaccct cagaagaaga acaacggatt      720
gaatcgcaac tgaaggatct tcttgaaaag gtgtgcactt tgaggccctc tagtccagcc      780
caacagacga tcatgctgac acgatccgat catagcgtga agccctcatc tcccagctct      840
cccgctctct tgactccgaa gccactotta ccgcattctg cctgaaacag agcaatcttg      900
cccgcaatcg cgaagtctct caggatcatc gccgcgaatt gcagcgcctg aacgccgcaa      960
tcgccgagtc ccgcgaccga gccaatcttc tgtctaacgt ccgctccgac attgatgcct     1020
accgcaattc aaacccccgcc gcggctgagg cagactacat gctcgaggag cgggggtcgt      1080
tagatgaaag ccataacatg atagatgggt tcctaagcca ggcgtagtga atcaacgaga     1140
gttttgggct acaacgtgaa accctggcca gcatcaatcg ccgtatcgtc ggtgctgcca     1200
ataaggtacc aggaatgaat gcattgattg gtaagattgg gacgaagagg agacgtgacg     1260
caatcatctt gggggctttt atcggctttt gtttcttgat ggtgttcttc ttccgatgag     1320
atgctggtgc tccgtatacc gccgatcttc ctgtgttata attccttgct caacgttatc     1380
tacatcggag accgcacggc gttcgggtgt ttctatgtac tccttttctg catgcaagca     1440
ctaatacaaa tggatcatggc gtttcagggt gtctatttca catttatgta catacagggt     1500
cagactgctg tagccctagg gctcaccgca tgatcactct tggtttcgga cttgcggatt     1560
caccttgggt tcttcccgcc cattcctcag ccggtagctt cgactcgaga ctgattcttc     1620
tctcctggat taatttgca accccgttgt tcaatccgtc tagctcgctt tectctgccg     1680
gcccgctacc cgcccatcgg atgcgacagt tctcgtccag cagatagaca taaccaactt     1740
tactgttcat cattccgatt gcttctttca acccatccgt aagaccttg cgcacaagga     1800
aataccgttc gtgctgctc

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<210> 156

<211> 819

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA263; clone 4-3-3; contig 4944 region 159432-161250
 Genomic sequence containing the coding region

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PCT/IB03/01374

```

<400> 156
atggcaactt cgactgggac cggatgggct cagctccggc agcaagcccg ttcgcttgag    60
actcaggtac ggaactcgaa actacgctat aatgaggctt tactcgtgat ttggatgttg    120
acaataatgt tcctagaccg agagtctgtt tcacacctat gcgcagtatg catcgatgac    180
gaagctgcct ccgaaaccct cagaagaaga acaacggatt gaatcgcaac tgaaggatct    240
tcttgaaaag gtgtgcactt tgaggccctc tagtccagcc caacagacga tcatgctgac    300
acgatccgat catagcgtga agccctcctc tcccagctct cccgtctcct tgactccgaa    360
gccactctta ccgcactctgc cctgaaacag agcaatcttg cccgcaatcg cgaagtcctc    420
caggatcatc gccgcgaatt gcagcgcttg aacgcgcgaa tcgccgagtc ccgcgaccga    480
gccaatcttc tgtctaactg ccgctccgac attgatgcct accgcaattc aaaccccgcc    540
gcggctgagg cagactacat gctcgaggag cggggctcgt tagatgaaag ccataacatg    600
atagatgggtg tcctaagcca ggcgtatgca atcaacgaga gttttgggct acaacgtgaa    660
accctggcca gcatcaatcg ccgtatcgtc ggtgctgcca ataaggtacc aggaatgaat    720
gcattgattg gtaagattgg gacgaagagg agacgtgacg caatcatctt gggggctttc    780
atcggtcttt gtttcttgat ggtgttcttc ttccgatga    819

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<210> 157
<211> 684
<212> DNA
<213> Aspergillus fumigatus

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<220>
<223> Phylum CEA263; clone 4-3-3; contig 4944 region 159432-161250
Coding region without introns

```

```

<400> 157
atggcaactt cgactgggac cggatgggct cagctccggc agcaagcccg ttcgcttgag    60
actcagaccg agagtctgtt tcacacctat gcgcagtatg catcgatgac gaagctgcct    120
ccgaaaccct cagaagaaga acaacggatt gaatcgcaac tgaaggatct tcttgaaaag    180
cgtgaagccc tcctctccca gctctcccggt ctccttgact ccgaagccac tcttaccgca    240
tctgccttga aacagagcaa tcttgcccgc aatcgcgaaag tcttcaggga tcatgcgcgc    300
gaattgcagc gccctgaacgc cgcaatcgcc gagtcccgcg accgagccaa tcttctgtct    360
aacgtccgct ccgacattga tgcctaccgc aattcaaacc ccgccgcggc tgaggcagac    420
tacatgctcg aggagcgggg tcgtatagat gaaagccata acatgataga tgggtgtccta    480
agccaggcgt atgcaatcaa cgagagtttt gggctacaac gtgaaaccct ggccagcatc    540
aatcgccgta tcgtcgggtg tgccaataag gtaccaggaa tgaatgcatt gattggtaag    600
attgggacga agaggagacg tgacgcaatc atcttggggg ctttcatcgg cttttgtttc    660
ttgatgggtg tcttcttccg atga    684

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<210> 158
<211> 227
<212> PRT
<213> Aspergillus fumigatus

```

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<220>
<223> Phylum CEA263; clone 4-3-3; contig 4944 region 159432-161250
Protein sequence

```

```

<400> 158

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Met Ala Thr Ser Thr Gly Thr Gly Trp Ala Gln Leu Arg Gln Gln Ala
1           5           10           15

Arg Ser Leu Glu Thr Gln Thr Glu Ser Leu Phe His Thr Tyr Ala Gln
20           25           30

Tyr Ala Ser Met Thr Lys Leu Pro Pro Lys Pro Ser Glu Glu Glu Gln
35           40           45

```

WO 03/076464

PCT/IB03/01374

Arg Ile Glu Ser Gln Leu Lys Asp Leu Leu Glu Lys Arg Glu Ala Leu
 50 55 60
 Ile Ser Gln Leu Ser Arg Leu Leu Asp Ser Glu Ala Thr Leu Thr Ala
 65 70 75 80
 Ser Ala Leu Lys Gln Ser Asn Leu Ala Arg Asn Arg Glu Val Leu Gln
 85 90 95
 Asp His Arg Arg Glu Leu Gln Arg Leu Asn Ala Ala Ile Ala Glu Ser
 100 105 110
 Arg Asp Arg Ala Asn Leu Leu Ser Asn Val Arg Ser Asp Ile Asp Ala
 115 120 125
 Tyr Arg Asn Ser Asn Pro Ala Ala Ala Glu Ala Asp Tyr Met Leu Glu
 130 135 140
 Glu Arg Gly Arg Ile Asp Glu Ser His Asn Met Ile Asp Gly Val Leu
 145 150 155 160
 Ser Gln Ala Tyr Ala Ile Asn Glu Ser Phe Gly Leu Gln Arg Glu Thr
 165 170 175
 Leu Ala Ser Ile Asn Arg Arg Ile Val Gly Ala Ala Asn Lys Val Pro
 180 185 190
 Gly Met Asn Ala Leu Ile Gly Lys Ile Gly Thr Lys Arg Arg Arg Asp
 195 200 205
 Ala Ile Ile Leu Gly Ala Phe Ile Gly Phe Cys Phe Leu Met Val Phe
 210 215 220
 Phe Phe Arg
 225

<210> 159

<211> 2601

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA264; contig 4899 region 65039-62439

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 159

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tcctgcctcc	ttttcgtctt	ctttttttcc	cctttttatc	ttttcatttt	atcatctttg	120
ttactgtttt	cccaaacgaa	tccattatta	tttctttccc	ttggagggtc	cctactgtgg	180
tcttgtgtct	gcactcttgc	caagcccat	ggtccttgct	ctgagcctat	cacttgcgat	240
tcgcccgcgc	ataagtccgc	ctctctcaac	ctttccatct	cacgcgcacc	tccactcaac	300
atccaccatt	cggatattcc	gcccatccaa	agcgaacacc	cctccttctg	ctccaccatc	360
gattgcagtc	tgcccaaaac	ggacttcaga	actcccttct	acgctatttt	ccgccattca	420
ctgttgaagt	gcagccctcc	atactctcga	tagcaactgc	ccaaccccc	tcttactgcc	480
aaccccacaa	gttgcccggtg	atgtcacaaa	atcgacctgg	ggtgttctcg	aatctgcgca	540
tgggtggtaa	ggaacatcca	aatgctgagt	ccaattgttc	agaaaacatt	acccaggagc	600
ctgtggaact	aactgctttg	ctttccgacc	atacagaagt	cgtccgcgag	aagggtccagg	660
atggactgac	aggggaaact	aaggagattt	cgtactcaca	atgtaaaatc	gtcggcaatg	720
gatcgtttgg	tgctgctctt	cagacgaaaa	tgatgccaa	cggcgaggat	gctgccatta	780
agagggctct	tcaagacaag	cgcttcaaag	tatgtgtaca	ttataagggc	aattgccctc	840

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PCT/IB03/01374

```

gctgcccac ccaaagatac tgtcgctgac gagataccag aatcgagaac tgcagattat 900
gcgatttggt cgccatccta acatcgtaga attgaaagcc ttctattact cgaacggcga 960
gagggtagtc gactctcctt tgtctcccca ttctgtctag ttgccggtt gctgactacc 1020
ctaccattgt ctttcacaga aggatgaagt gtacctaaac ctctgtctcg aatacgtaac 1080
agaaaccgtg tatcgggcgt cgcggtactt taataaaactc aaaacgacta tgccaatggt 1140
ggaagtcaag ctgtatatct atcaattggt ccgttccctg gcatacatcc attcacaagg 1200
catctgccac cgtgacatca agccccagaa tctcttactt gatccatcca ccggcatcct 1260
caaactctgc gactttgggt cggccaagat tctggtagag aatgagccca acgtttccta 1320
tatctgttcc cgctactatc gtgcgcggga attgatcttt ggccgccaata attacacaac 1380
aaagatcggt aagtccttgac tgattcctcc ttcaagtttg gtactgtcat gctgacgatc 1440
gtcaagacgt gtggtccacg ggttggtgta tggctgaact catgcttggt cagccattgt 1500
tccctggaga gtcgggaatt gaccaactgg tggaaatcat caaggttctt ggaacccta 1560
ctcgggagca gatccgcacc atgaacccaa actatatgga gcacaaattc cctcaaatca 1620
agccacaccc attcaacaag gtgaccacgc tcttaaagaa cttcttgcca atatgcactg 1680
acttgatgac cccaggtttt ccggagagct cctcacgagg ccattgatct gatctcagct 1740
ttgtagaatt acacgcccag acaacgtctc tccgctatcg agcgatgtg ccaccggtc 1800
ttcgacgaac tcagagatcc caatacgcga ctgcccgaact ctcgccaccc tgggtggcgt 1860
gctagagacc tccccaatct ctttgatttc tccagacatg gtttggtgtc acttgaggcc 1920
caaattcatt cttccagatg gcttattcgc tgatcactct tttgtagaac tttctattgc 1980
acctgcattg aacagccggc tggttccccc tcatgcacgc gccgctctcg aggccgggg 2040
gctagacatt gacaacttca ctctctcac gaaggaggag atgatggcac gtctcgactg 2100
agtcgatacg tttctcgtaa cgaatcaaac gccccctcga tagtgcttat atccgcacaa 2160
ctgcgcgagg atatgatgtc atgcatgca ttttgctttg tgaactggga tgccttgga 2220
ccagaagtgg cttttatgga acttgctcgc cagagtcgct gactagacac ccgggagttg 2280
gcacttttcc cgaacgtatg aggatacaag gcaaatcccc atatttaaaa gaaaaaggag 2340
aaaaacaggag aaaaaaaagg aatgggaaat acagaaacat cgacttctgg tcacaacata 2400
agcggtttcc gtgagcggtt ggtgcatcat gacaatatca tgcaacgggg ttgaggaatt 2460
gtcatagtct ggagtttctg aggtgtctga gacagctctt gggaaaggaa aaaaagtgat 2520
acccttagt gtgcgagctt gccttcgggg atttaagttt gcatagcttc attctcgttt 2580
gaaggaggac atgaccattc c 2601

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<210> 160

<211> 1601

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA264; contig 4899 region 65039-62439
 Genomic sequence containing the coding region

<400> 160

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atgtcacaaa atcgacctgg ggtgttctcg aatctgcgca tgggtggtaa ggaacatcca 60
aatgctgagt ccaattgttc agaaaacatt acccaggagc ctgtggaact aactgctttg 120
ctttccgacc atacagaagt cgcccgcgag aagggtccagg atggactgac aggggaaact 180
aaggagattt cgtactcaca atgtaaaatc gtcggcaatg gatcgtttg tgcgtcttt 240
cagacgaaaa tgatgccaag cggcgaggat gctgccatta agagggctct tcaagacaag 300
cgcttcaaa g tatgtgtaca ttataagggc aattgccttc gctgcccac ccaaagatac 360
tgtcgtgac gagataccag aatcgagaac tgcagattat gcggattgtt cgccatccta 420
acatcgtaga attgaaagcc ttctattact cgaacggcga gagggtagtc gactctcctt 480
tgtctcccca ttctgtctag ttgcccgttt gctgactacc ctaccattgt ctttcacaga 540
aggatgaagt gtacctaaac ctctgtctcg aatacgtaac agaaaccgtg tatcgggcgt 600
cgcggtactt taataaaactc aaaacgacta tgccaatggt ggaagtcaag ctgtatatct 660
atcaattggt ccgttccctg gcatacatcc attcacaagg catctgccac cgtgacatca 720
agccccagaa tctcttactt gatccatcca ccggcatcct caaactctgc gactttgggt 780
cggccaagat tctggtagag aatgagccca acgtttccta tatctgttcc cgctactatc 840
gtgcgcggga attgatcttt ggccgccaata attacacaac aaagatcggt aagtccttgac 900
tgattcctcc ttcaagtttg gtactgtcat gctgacgatc gtcaagacgt gtggtccacg 960
ggttggtgta tggctgaact catgcttggt cagccattgt tccctggaga gtcgggaatt 1020
gaccaactgg tggaaatcat caaggttctt ggaacccta ctcgggagca gatccgcacc 1080
atgaacccaa actatatgga gcacaaattc cctcaaatca agccacaccc attcaacaag 1140

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PCT/IB03/01374

```

gtgaccacgc tcttaaagaa cttcttgcca atatgcactg acttgatgac cccagggttt 1200
ccggagagct cctcacgagg ccattgatct gatctcagct ttgctagaat acacgccgac 1260
acaacgtctc tccgctatcg aggcgatgtg ccacccgttc ttcgacgaac tcagagatcc 1320
caatacgcga ctgcccgact ctccggcacc tggtggcgct gctagagacc tccccaatct 1380
ctttgatttc tccagacatg gtttgtgtc acttgaggcc caaattcatt cttccagatg 1440
gcttattcgc tgatcactct tttgtagaac tttctattgc acctgcattg aacagccggc 1500
tggttcccc tcatgcacgc gccgctctcg aggccgggg gctagacatt gacaacttca 1560
ctcctctcac gaaggaggag atgatggcac gtctcgactg a 1601

```

<210> 161

<211> 1185

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA264; contig 4899 region 65039-62439

Coding region without introns

<400> 161

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atgtcacaaa atcgacctgg ggtgttctcg aatctgcgca tgggtgaagt cgtccgagag 60
aagggtccagg atggactgac aggggaaact aaggagattt cgtactcaca atgtaaaatc 120
gtcggcaatg gatcgtttgg tgcgtcttt cagacgaaaa tgatgccaaag cggcgaggat 180
cgtgccatta agagggctct tcaagacaag cgcttcaaaa atcgagaact gcagattatg 240
ggattgttgc gccatcctaa catcgtagaa ttgaaagcct tctattactc gaacggcgag 300
aggaaggatg aagtgtacct aaacctcggt ctccaatacg taccagaaac cgtgtatcgg 360
gcgtcgcggt actttaataa actcaaaacg actatgccaa tgttggaagt caagctgtat 420
atctatcaat tgttccgttc cctggcatac atccattcac aaggcatctg ccaccgtgac 480
atcaagcccc agaattctct acttgatcca tccaccggca tctcaaaact ctgcgacttt 540
ggttcggcca agattctggg agagaatgag cccaacgttt cctatatctg tccccgtac 600
tatcgtgcgc cggaattgat ctttggcgcc actaattaca caacaaagat cgacgtgtgg 660
tccacgggtt gtgtgatggc tgaactcatg cttggtcagc cattgttccc tggagagtcg 720
ggaattgacc aactggtgga aatcatcaag gttcttggaa cccctactcg ggagcagatc 780
cgcaccatga acccaacta tatggagcac aaattccctc aaatcaagcc acaccattc 840
aacaagggtt tccggagagc tctcacgag gccattgatc tgatctcagc tttgctagaa 900
tacacgccga cacaacgtct ctccgctatc gaggcgatgt gccaccgtt cttcgacgaa 960
ctcagagatc ccaatacgcg actgcccagc tctcggcacc ctggtggcgc tgctagagac 1020
ctcccgaatc tctttgattt ctccagacat gaactttcta ttgcacctg attgaacagc 1080
cggctgggtc cccctcatgc acgcgccgct ctcgaggccc gggggctaga cattgacaac 1140
ttcactcttc tcacgaagga ggagatgatg gcacgtctcg actga 1185

```

<210> 162

<211> 394

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA264; contig 4899 region 65039-62439

Protein sequence

<400> 162

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Met Ser Gln Asn Arg Pro Gly Val Phe Ser Asn Leu Arg Met Gly Glu
1          5          10          15

```

```

Val Val Arg Glu Lys Val Gln Asp Gly Leu Thr Gly Glu Thr Lys Glu
20          25          30

```

```

Ile Ser Tyr Ser Gln Cys Lys Ile Val Gly Asn Gly Ser Phe Gly Val
35          40          45

```

WO 03/076464

PCT/IB03/01374

Val Phe Gln Thr Lys Met Met Pro Ser Gly Glu Asp Ala Ala Ile Lys
 50 55 60
 Arg Val Leu Gln Asp Lys Arg Phe Lys Asn Arg Glu Leu Gln Ile Met
 65 70 75 80
 Arg Ile Val Arg His Pro Asn Ile Val Glu Leu Lys Ala Phe Tyr Tyr
 85 90 95
 Ser Asn Gly Glu Arg Lys Asp Glu Val Tyr Leu Asn Leu Val Leu Glu
 100 105 110
 Tyr Val Pro Glu Thr Val Tyr Arg Ala Ser Arg Tyr Phe Asn Lys Leu
 115 120 125
 Lys Thr Thr Met Pro Met Leu Glu Val Lys Leu Tyr Ile Tyr Gln Leu
 130 135 140
 Phe Arg Ser Leu Ala Tyr Ile His Ser Gln Gly Ile Cys His Arg Asp
 145 150 155 160
 Ile Lys Pro Gln Asn Leu Leu Leu Asp Pro Ser Thr Gly Ile Leu Lys
 165 170 175
 Leu Cys Asp Phe Gly Ser Ala Lys Ile Leu Val Glu Asn Glu Pro Asn
 180 185 190
 Val Ser Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala Pro Glu Leu Ile Phe
 195 200 205
 Gly Ala Thr Asn Tyr Thr Thr Lys Ile Asp Val Trp Ser Thr Gly Cys
 210 215 220
 Val Met Ala Glu Leu Met Leu Gly Gln Pro Leu Phe Pro Gly Glu Ser
 225 230 235 240
 Gly Ile Asp Gln Leu Val Glu Ile Ile Lys Val Leu Gly Thr Pro Thr
 245 250 255
 Arg Glu Gln Ile Arg Thr Met Asn Pro Asn Tyr Met Glu His Lys Phe
 260 265 270
 Pro Gln Ile Lys Pro His Pro Phe Asn Lys Val Phe Arg Arg Ala Pro
 275 280 285
 His Glu Ala Ile Asp Leu Ile Ser Ala Leu Leu Glu Tyr Thr Pro Thr
 290 295 300
 Gln Arg Leu Ser Ala Ile Glu Ala Met Cys His Pro Phe Phe Asp Glu
 305 310 315 320
 Leu Arg Asp Pro Asn Thr Arg Leu Pro Asp Ser Arg His Pro Gly Gly
 325 330 335
 Ala Ala Arg Asp Leu Pro Asn Leu Phe Asp Phe Ser Arg His Glu Leu
 340 345 350
 Ser Ile Ala Pro Ala Leu Asn Ser Arg Leu Val Pro Pro His Ala Arg
 355 360 365

WO 03/076464

PCT/IB03/01374

Ala Ala Leu Glu Ala Arg Gly Leu Asp Ile Asp Asn Phe Thr Pro Leu
 370 375 380

Thr Lys Glu Glu Met Met Ala Arg Leu Asp
 385 390

<210> 163
 <211> 2539
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA265; clone 11-4-9; contig 4826 region 355652-358190
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 163
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 ttggagatag caagagacgt gcaggcagca tccttgggtga catccagatc gaggaggagg 120
 gcgctgtggc atggcgatcc gatcaggag atgatgacat cgtggacagg ttgtgggaga 180
 gcggacgaga taggacggag aacgggttga agagggtcaa taacgaccct ttgaagcgta 240
 tccatggcga gagtctacag ggcaaaagac ggctcagggc cttgggttgaa gaggagtgtg 300
 ccaacggagc acggtggttc caaaagatca gcaacaacca tcgggacgga atggtgcatt 360
 cattcctgcg gttgtggtct ctgtgcctcg cgggggaatt tctgccctgt caatcgcgac 420
 tcttccgaga ctactatct catgatctag atatcgtcct atcgtgattt caatatccct 480
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WO 03/076464

PCT/IB03/01374

<210> 164
 <211> 1539
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA265; clone 11-4-9; contig 4826 region 355652-358190
 Genomic sequence containing the coding region

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 gagcgcaaga tgatacctgc gaagacgagt agctcgtga 1539

<210> 165
 <211> 1539
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA265; clone 11-4-9; contig 4826 region 355652-358190
 Coding region without introns

<400> 165
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gcgctctccg ccagtaatat ctgtctctat gcctttgtgt atacgccgct gaagcgata      900
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gccaacggca gtgctcgacg cctcttctgg gccagtattt ggcagctgcc aatcctcctt     1380
gtcggtggtc tggtcacgaa gaaagggtct tgggatgggt tctggaacaa tgttttcggt     1440
cagcctgtgg aagacgagga tgactatctc tgggaggatg aggatgaagt ggcagaggcg     1500
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<210> 166

<211> 512

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA265; clone 11-4-9; contig 4826 region 355652-358190
Protein sequence

<400> 166

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Arg Pro Val Ala Val Arg Ser Phe Phe Ser Ser Ser Arg Leu Arg Ala
          35           40           45

Gly Ile Ala Asp His Glu Ser Thr Pro Ser Thr Val Gln Lys Thr Tyr
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Phe Ser Ala Asn Arg Thr Ala Asp Gly Leu Leu Ala Ser Leu Ser Ala
          65           70           75           80

Val Asn Ser Ser Pro Arg Ser Ile Ala Asp Asn Ala Leu Ser Gln Gly
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Ala Ala Ser Ser Glu Ser Ile Thr Ser Gln Ser Thr Ser Gln Glu Leu
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Pro His Arg Arg Arg Lys Arg Leu Lys Glu Glu Ala Ala Lys Asn Asn
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Leu Ser Ser Ala Leu Pro Ala Thr Ser Leu Arg Arg Lys Leu Ala Ala
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Phe Leu Ala Leu Thr Lys Pro Arg Leu Ser Phe Leu Ile Val Leu Thr
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Thr Thr Ser Ala Tyr Gly Met Tyr Pro Ile Ser Ser Leu Leu Thr Leu

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Thr	Leu	Asn	Met	Leu	Leu	Glu	Pro	Lys	Tyr	Asp	Ala	Leu	Met	Ser	Arg
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	370					375					380				
Asn	Pro	Ala	Ala	Asn	Ala	Arg	Val	Ala	Leu	Arg	Tyr	Ser	Leu	Leu	Met
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Phe	Pro	Phe	Ser	Val	Gly	Leu	Trp	Trp	Val	Gly	Val	Val	Gly	Asn	Gly
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		435					440					445			
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Gln	Pro	Val	Glu	Asp	Glu	Asp	Asp	Tyr	Leu	Trp	Glu	Asp	Glu	Asp	Glu
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WO 03/076464

PCT/IB03/01374

<210> 167
<211> 2679
<212> DNA
<213> *Aspergillus fumigatus*

<220>
<223> Phylum CEA266; clone 2-10-18; contig 4898 region 329309-331987
Genomic sequence containing 3' and 5'-ends and the coding region

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<210> 168
<211> 1629

WO 03/076464

PCT/IB03/01374

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA266; clone 2-10-18; contig 4898 region 329309-331987
 Genomic sequence containing the coding region

<400> 168

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gcgacctag						1629

<210> 169

<211> 1629

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA266; clone 2-10-18; contig 4898 region 329309-331987
 Coding region without introns

<400> 169

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gatgccgttt	cgcgtctcga	cgcggagatc	cgcgctcttg	agctctacat	gacaccgacc	600
ccgtcggagc	ggactgagat	agatcggctg	gttgagata	tgggtagggt	gctagcggga	660
atcgccccca	gccccccca	ggtaaccggt	tcatggcgga	cgcgatttgc	cttgagccac	720
tcgggtctcg	attttgtctt	acctgtcccg	gattcagacc	gatccaccgg	tgacgttcgc	780

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aagccgagtg ccacacggcc caaggtgctc cagacttaca aaaagctctt acatgaagtg      840
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ttccccgtcc tctcagccat ccacgcgcc acgggcccgc tgctgcagtt ccactgcggt      960
gaagggtac cgccctctgt cgaatacatc atggattacc aggcagagta tccctcgatc     1020
cggccgctct acgtgaccgc tcgcctgac ctggaggcgc ggggtaggta tggccgtact     1080
cagatgtcta ttgaatccga tgccctcgta atgcttctcg tggccttcct caaaatgaac     1140
cacggcggtt ttcagcggcc cgactgtctc ggcgagcagc tgatcgcggt tctgcgcgcc     1200
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aatgctagta cgggtcaaacg cgccagcgcc ctgtacgcgc ccgatgatct acccgcgcat     1320
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gcaagtctca aqcgctggga tgacagtga cggccgcga acgttagtat cctgacacgg     1560
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<210> 170

<211> 542

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA266; clone 2-10-18; contig 4898 region 329309-331987
Protein sequence

<400> 170

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Ala Pro Leu Phe Ser Thr Ala Pro Phe Arg Arg Gln Leu His Ala Ser
          35              40              45

Gly Val Arg Ser Ile Glu Pro Val Ile Phe Arg Asn Ser Leu Glu Lys
          50              55              60

Thr Leu Glu Ala His Arg Ser Ser Asn Arg Ala Ser Leu Ile Arg Lys
          65              70              75              80

Val Ile Asn His Asp Cys Pro Ala Glu Thr Pro Pro Pro Ile Leu Pro
          85              90              95

Leu Glu Asn Arg Ala Gly His Asp Gln Ser Ser Gln Lys Ala Ser Ser
          100             105             110

Val Ser Asn Ala Glu Ser Glu Ser Pro Arg Ser Ser Ala Pro Ala Arg
          115             120             125

Arg Ala Gln Arg Lys Ala Arg Ser Pro Ser Gln Val Ala Thr Pro Gln
          130             135             140

Pro Gln Thr Thr Glu Tyr Pro Gln Leu Gln Trp His Ala Asp Glu Thr
          145             150             155             160

Lys Gly Arg Pro Ala Gln Ser Pro Trp Leu Lys Tyr Leu Thr Thr Asp
          165             170             175

Trp Lys Thr Pro Asp Ala Val Ser Arg Leu Asp Ala Glu Ile Arg Ala

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Leu	Glu	Leu	Tyr	Met	Thr	Pro	Thr	Pro	Ser	Glu	Arg	Thr	Glu	Ile	Asp		
		195					200					205					
Arg	Leu	Val	Ala	Asp	Met	Gly	Arg	Leu	Leu	Ala	Gly	Ile	Val	Pro	Ser		
	210					215					220						
Pro	Pro	Gln	Val	Thr	Gly	Ser	Trp	Arg	Thr	Arg	Phe	Ala	Leu	Ser	His		
225					230					235					240		
Ser	Gly	Leu	Asp	Phe	Val	Leu	Pro	Val	Pro	Asp	Ser	Asp	Arg	Ser	Thr		
				245					250					255			
Arg	Asp	Val	Arg	Lys	Pro	Ser	Ala	Thr	Arg	Pro	Lys	Val	Leu	Gln	Thr		
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Tyr	Lys	Lys	Leu	Leu	His	Glu	Val	Gly	His	Ala	Leu	Gln	Gln	Ser	Pro		
	275						280					285					
Ser	Phe	Ala	Glu	Arg	Val	Arg	Ile	Ile	Gly	Ser	Arg	Phe	Pro	Val	Leu		
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305					310					315					320		
Glu	Gly	Leu	Pro	Ala	Ser	Val	Glu	Tyr	Ile	Met	Asp	Tyr	Gln	Ala	Glu		
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Tyr	Pro	Ser	Ile	Arg	Pro	Leu	Tyr	Val	Thr	Ala	Arg	Leu	Ile	Leu	Glu		
			340					345					350				
Ala	Arg	Gly	Arg	Tyr	Gly	Arg	Thr	Gln	Met	Ser	Ile	Glu	Ser	Asp	Ala		
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Leu	Val	Met	Leu	Leu	Val	Ala	Phe	Leu	Lys	Met	Asn	His	Gly	Arg	Phe		
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Gln	Arg	Pro	Asp	Cys	Leu	Gly	Glu	Gln	Leu	Ile	Ala	Phe	Leu	Arg	Ala		
385					390					395					400		
Tyr	Gly	Ser	Asp	Ile	Asp	Leu	Thr	Thr	Thr	Gly	Val	Ser	Val	Asp	Pro		
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Pro	Ser	Trp	Phe	Asn	Ala	Ser	Thr	Val	Lys	Arg	Ala	Ser	Ala	Leu	Tyr		
			420					425					430				
Ala	Pro	Asp	Asp	Leu	Pro	Ala	His	Leu	Arg	Gly	Gln	Arg	Ser	Leu	Ile		
		435					440					445					
Ser	Leu	Lys	Arg	Thr	Ala	Ala	Ala	Arg	Arg	Asn	Leu	Pro	Ala	Ala	Ser		
	450					455					460						
Arg	Leu	Cys	Val	Gln	Asp	Pro	Thr	Asn	Tyr	Met	Asn	Asp	Leu	Gly	Arg		
465					470					475					480		
Ser	Cys	Val	Arg	Thr	Leu	Glu	Leu	Gln	His	Thr	Phe	Ser	Leu	Ala	His		
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Asp	Arg	Leu	Gly	Ala	Ser	Leu	Lys	Arg	Trp	Asp	Asp	Ser	Glu	Pro	Ala		
			500					505					510				

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Ala Asn Val Ser Ile Leu Thr Arg Ala Leu Gln Ala Asn Phe Ser Asp
 515 520 525

Phe Glu Asn Leu Arg Ala Lys Ser Leu Lys Leu Asn Ala Thr
 530 535 540

<210> 171

<211> 1573

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA280; clone 6-8-13; contig 4925 region 997952-996381
 Genomic sequence containing 3' and 5'-ends and the coding region

<220>

<223> misc_feature

<223> (683)..(683)

<223> n is a, c, g, or t

<400> 171

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ccatgtcaac	cacgaggatt	cagtctctgc	ctcatctcag	tccaggcgag	gtttctttgc	240
tggatctttg	ggctgatgac	cctcgcgatg	tggtgtccct	gtccgacaag	gaagcgttga	300
ttttgcagct	ctacaatcaa	atccaggaac	tggaactgga	aaaggcactt	cttgaacaag	360
gtacgcgtca	aatttatttt	ttttgtaatt	ttcttttttt	tgtttctctg	atgtagcttc	420
ttggggcctc	caaactctgtc	agcccagggt	actgattccc	actagagctg	gaaccggctt	480
ctgggggaaa	tctggatgag	caacttgcaa	tgcgagaacg	tgagcttctc	gaggcaaggg	540
ccacgtacac	ggtcaggaga	aaggccacca	gtactgtcct	gatgactgat	ccaacattaa	600
aagctgttca	cttgaaagct	atatcacctg	ttgaaagggt	ttacctcctt	tcagtttatg	660
cgagcatttc	aattctgcat	tcnctatac	taacgcttca	tagagctctt	ctacccttgg	720
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caagatggga	agtcatgaaa	agcgttgcaa	gtgctattgt	tgtgggaagt	ggagtgaact	1020
gggctgaaga	cgatgagctt	acagctctag	tcattgatga	atctgatgat	taaataatcg	1080
cctcgaaaatt	aatgatattcg	aacaatttgg	tagtattgac	ttctccgacc	ggcgacttac	1140
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cggtatatac	acagtatcgt	cttggtcgaa	tcagcagaac	ggctgaggaa	gtcgggttag	1260
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<210> 172

<211> 573

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA280; clone 6-8-13; contig 4925 region 997952-996381
 Genomic sequence containing the coding region

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<220>
 <223> misc_feature
 <223> (183)..(183)
 <223> n is a, c, g, or t

<400> 172
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 atatcacctg ttgaaagggt ttacctcctt tcagtttatg cgagcatttc aattctgcat 180
 tcncctatac taacgcttca tagagctctt ctacccctgg tcaaccggcg tgatgtgttg 240
 tctttggcac atgagaacct aatgaatgcg cacaacgcga ctttgaggga actatccaat 300
 ttagaagtac aaaatctaga gctacaccag aggaatcaag agctagcgcg gcagcttctt 360
 gagtccgcga aggatgatga ttcattggaga gaagcactgg atgatgacga cctcaaggca 420
 caacttgagc agctagaggc cgatcgcaaa aagagcaaat caagatggga agtcatgaaa 480
 agcgttgcaa gtgctattgt tgtgggaagt ggagtgaact gggctgaaga cgatgagctt 540
 acagctctag tcattgatga atctgatgat taa 573

<210> 173
 <211> 573
 <212> DNA
 <213> Aspergillus fumigatus

<220>
 <223> Phylum CEA280; clone 6-8-13; contig 4925 region 997952-996381
 Coding region without introns

<220>
 <223> misc_feature
 <223> (183)..(183)
 <223> n is a, c, g, or t

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 atatcacctg ttgaaagggt ttacctcctt tcagtttatg cgagcatttc aattctgcat 180
 tcncctatac taacgcttca tagagctctt ctacccctgg tcaaccggcg tgatgtgttg 240
 tctttggcac atgagaacct aatgaatgcg cacaacgcga ctttgaggga actatccaat 300
 ttagaagtac aaaatctaga gctacaccag aggaatcaag agctagcgcg gcagcttctt 360
 gagtccgcga aggatgatga ttcattggaga gaagcactgg atgatgacga cctcaaggca 420
 caacttgagc agctagaggc cgatcgcaaa aagagcaaat caagatggga agtcatgaaa 480
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 acagctctag tcattgatga atctgatgat taa 573

<210> 174
 <211> 190
 <212> PRT
 <213> Aspergillus fumigatus

<220>
 <223> Phylum CEA280; clone 6-8-13; contig 4925 region 997952-996381
 Protein sequence

<400> 174

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 Thr Val Arg Arg Lys Ala Thr Ser Thr Val Leu Met Thr Asp Pro Thr
 20 25 30

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[illegible]

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PCT/IB03/01374

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ccgactagtc	tgggagacca	acgagttaga	ccctattcat	caggagaaaa	aggacgatgg	2040
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aagctggagg	gcaacactga	ctgctgtttt	aggactaggt	cggttttggg	tggcagatta	2520
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<210> 176

<211> 1974

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.1; clone 5-3-11; contig 4839 region 10030-12622
Genomic sequence containing the coding region

<400> 176

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gtattttcaa	gactggatag	agcggattga	ctgacttgaa	cggaggtag	aaggaaacac	240
cccacggctg	gttcgttcgt	gcgccttcg	cgacggaccg	acagacctcg	aggcttcctt	300
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aagttcatca gaagagaggt tgagctcctg gattcaacgc gagacatagg cttttggttc 1920
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<210> 177

<211> 1830

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.1; clone 5-3-11; contig 4839 region 10030-12622
Coding region without introns

<400> 177

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cccacgcggg ggaagcattc tggagaacac aacggagtga gatattttac atgtagaagg 180
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ctcaactaca gcaagataac ttccaagac cgaagtaatg gcgaactcta ttacctttcc 1260
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<210> 178

<211> 609

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.1; clone 5-3-11; contig 4839 region 10030-12622

WO 03/076464

PCT/IB03/01374

Protein sequence

<400> 178

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Met Asp Val Gly Cys Phe Val Asn Gln Arg Arg Ser Tyr Asn Gly Asp
1      5      10      15
Leu Cys Thr Val Arg Tyr Ile Gly Lys Val Glu Gly Thr Thr Gly Glu
20      25      30
Trp Leu Gly Val Glu Trp Asp Asp Pro Thr Arg Gly Lys His Ser Gly
35      40      45
Glu His Asn Gly Val Arg Tyr Phe Thr Cys Arg Arg Lys His Pro Thr
50      55      60
Ala Gly Ser Phe Val Arg Pro Ser Arg Arg Thr Asp Arg Pro Arg Gly
65      70      75      80
Phe Leu Glu Ala Val Arg His Lys Tyr Ala Ser Glu Phe Gln Glu Glu
85      90      95
Leu Ala Arg Gln Gln Ser Gly Glu Val Ser Ala Ala Arg Glu Ile Ile
100     105     110
Lys Phe Ser Ser Lys Val Val Glu Glu Val Gly Phe Asp Lys Ile Arg
115     120     125
Lys Lys Leu Ala Glu Leu Gln Glu Leu Lys Ile Val Leu Leu Asp Arg
130     135     140
Leu Cys Ile Ala Gly Val Leu Pro His Arg Ala Ser Leu His Glu Leu
145     150     155     160
Ala Glu Ala Cys Lys Glu Ile Glu Gln Thr Cys Pro Lys Ile Val Asp
165     170     175
Leu Asp Leu Ser Tyr Asn Leu Leu Glu Ser Trp Val Asp Ile Ala Asn
180     185     190
Ile Cys Gln Gln Leu Lys Arg Leu Lys Thr Leu Lys Leu Met Leu Val
195     200     205
Ile Gln Tyr Ile Cys Glu Lys His Ala Asp Ser Trp Gln Arg Lys Ser
210     215     220
Ser Arg Ser Ser Thr Gly Gly Ser Asp Ile Arg Arg Tyr His Asn Thr
225     230     235     240
Thr Leu Gly Arg Asp Ser Thr Arg Met Gly Arg Gly Met Leu His Lys
245     250     255
Ala Thr Ala Trp Leu Pro Ile Thr Gln Ile Leu Thr Pro Ile Thr Asp
260     265     270
Thr Ile Thr Thr Leu Thr Leu Glu Asn Asn Asp Ile Ser Ser Leu Ser
275     280     285
Ser Leu Ala Cys Leu Thr Ser Leu Ser Lys Leu Glu His Leu Ser Leu
290     295     300

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Arg Glu Asn Arg Ile Gly Lys Val Tyr Ala Ser Gly Met Glu Gly Asn
 305 310 315 320
 Ser Leu Gln Phe Ser Glu Asn Leu Arg Ser Val Asp Leu Ser Arg Asn
 325 330 335
 Asn Ile Asp Ser Trp Leu Phe Val Asn Glu Leu Gln Arg Val Phe Pro
 340 345 350
 Gly Leu Gln Ser Leu Arg Ile Ser Gly Asn Pro Leu Tyr Asp Lys Pro
 355 360 365
 Val Ala Pro Ser Asn Val Thr Asn Leu Pro Glu Lys Pro Met Thr Val
 370 375 380
 Asp Glu Ala Tyr Met Leu Thr Leu Ser Arg Leu Ala Ser Ile Gln Thr
 385 390 395 400
 Leu Asn Tyr Ser Lys Ile Thr Ser Gln Asp Arg Ser Asn Gly Glu Leu
 405 410 415
 Tyr Tyr Leu Ser Leu Ile Gly Lys Glu Leu Ser Ala Tyr Pro Glu Ser
 420 425 430
 Ala Glu Arg Glu Ile Leu Ala Thr His Pro Arg Tyr Gln Glu Leu Cys
 435 440 445
 Glu Lys Tyr Gly Ala Pro Thr Ile Arg Arg Ala Glu Leu Ala Gly Ala
 450 455 460
 Ala Val Asn Pro Arg Ser Val Ala Ala Arg Val Val Lys Leu Ala Phe
 465 470 475 480
 Cys Leu His Ser Ser Val Ser Ser Gly Ala Asn Gln Glu Gln Phe Arg
 485 490 495
 Val Gln Lys Ile Pro Arg Ser Phe Asn Thr Tyr Gln Val Lys Ala Ile
 500 505 510
 Ala Ser Arg Leu Phe Asn Leu Pro Pro Tyr Gln Cys Arg Leu Val Trp
 515 520 525
 Glu Thr Asn Glu Leu Asp Pro Ile His Gln Glu Lys Lys Asp Asp Gly
 530 535 540
 Asp Asp Trp Asp Ser Asp Glu Asp Glu Ala Thr Ala Ile Gly Leu Gly
 545 550 555 560
 Glu Ser Asn Lys Leu Thr Pro Ala Thr Glu Asp Gly Lys Phe Ile Arg
 565 570 575
 Arg Glu Val Glu Leu Leu Asp Ser Thr Arg Asp Ile Gly Phe Trp Phe
 580 585 590
 Gln Pro Asp Thr Val Glu Ala Arg Ile Arg Val Glu Val Ala Thr Ser
 595 600 605

Asn

<210> 179

WO 03/076464

PCT/IB03/01374

<211> 1867

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.2; clone 5-3-11; contig 4839 region 12269-14135
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 179

caactatttc	gacataggag	ttgtgaagga	gttccttaac	ctacattgtc	gcgggtgggg	60
taatatatat	agttgagcac	gactcgtgcg	ttaggataca	acgaggtcaa	cgacagaaaa	120
gtagaacctc	ttacgcaagc	gcctgtggcc	tctgttacct	gaatggattt	agaggccttc	180
ttggttattc	ttaaacaata	tgatatgtgt	agtgtatatt	caagctggag	ggcaacactg	240
actgctgttt	taggactagg	tcggttttgg	gtggcagatt	atcaccgcaa	ctgttttgtg	300
ataacagtga	tatcatttcc	ctttcatata	acaatttaac	actcagacat	cgatcatggca	360
gaatactgga	aatcagctgt	aagtgcacct	cattcagttc	cgagacttc	ttcgtgataa	420
tctttacgtg	gggaagtccg	gcatcaactg	acagcaatat	tctagccccg	gttctgggtgc	480
aaacaatgca	agatatccat	tcgggataca	cccttcgaga	aaaccagca	tgaagcgagt	540
gccaaacacc	agggaacact	taagcgtttc	ctacgagata	tccaccggga	aaatgaacgg	600
aagcaaagag	aaactcagaa	ggcgaaggat	gaagtcgagc	gattaaggca	aactgtcgcga	660
ggaaaaccag	gtgcaaaaaga	cagcggcgca	acagcttgga	aacacgcctc	ggctgcccct	720
ccaccggcag	aacgacctgt	gtccctggaa	gagagaaaaga	agcagatagc	gcagctggca	780
gagatgggaa	ttgctatccc	ggacgaatac	cgtggtgaac	tcgcgctcgc	tggcgaatgg	840
cagacggtat	ccgaacgagt	tattcgacca	gatgacgata	cagagggaag	aaagcctggt	900
agctctatcg	gcgttcggaa	acgcaagatg	gaaggcgatg	aggaggagca	ggaggcgcgca	960
caggaggccg	agagattcgt	gagtcagggt	tggggctcga	ggactcggca	gtatcctggg	1020
gagcagagcg	atgcagacct	ggatgcactt	ctaaattcta	ccaaggatgt	aaagaaggtc	1080
aagttgtcgg	cgccggatga	agggtcgaaa	gagaaggcta	gcaaagaggg	tgctacacca	1140
agcaacgata	cggaccaggc	tgccggtcag	gagtcagaac	taccatcagt	caagtctgag	1200
ggtaaagaag	cggcgcagct	tgctacaaca	gataccccag	cgggtgaagca	ggaagaggag	1260
gcggcaccta	caggagtgtg	ttttaagaag	cgcaagccga	aggctcctgag	gaaatagtcg	1320
aatattgcagc	tgctggatat	ctattatcta	ccatgcgcac	aaatgtacag	atgatgcgtt	1380
atggttgctc	acggtccaat	atgcctcgcc	tgcgggtgct	cacatgaagc	gatcatgggt	1440
tcttgtctca	ctgcgctcca	gtgttcgaaa	accgggatga	tgccctctggc	ctccagtcgt	1500
ccgtcgccga	agcaacccag	ctcatagaag	atctggattc	tcgattcgct	tgccgagaaa	1560
gcctagtctg	gtcttgcggt	agcctatctc	cagattgagt	gtatcgattc	gagcttatgc	1620
gggttgctctg	ataatattct	gccttacatt	ggcagagaga	cgttgagca	catagggtgg	1680
atggagaatg	atcagttcct	acgtatgtaa	gcatgatgtc	tagctcagaa	aagagtccca	1740
tataccatgc	gactcgttgg	cagcatccac	ctcttccttt	ggagtgcgat	ctacaatagc	1800
atgcatacga	aacaaatttc	gttgacaagg	agaccagggg	cgagaagagt	aatatagcaa	1860
gccagct						1867

<210> 180

<211> 963

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.2; clone 5-3-11; contig 4839 region 12269-14135
 Genomic sequence containing the coding region

<400> 180

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tgataatctt	tacgtgggga	agtcggcat	caactgacag	caatattcta	gccccgggtc	120
tggtgcaaac	aatgcaagat	attcattcgg	gataaccct	tcgagaaaac	ccagcatgaa	180
gcgagtgcc	aacaccaggg	aaaccttaag	cgtttcctac	gagatatcca	ccgggaaaat	240
gaacggaagc	aaagagaaac	tcagaaggcg	aaggatgaag	tcgagcgatt	aaggcaaac	300
gtccgaggaa	aaccagggtc	aaaagacagc	ggcgcaacag	cttggaacaa	cgctcggct	360
gcccctccac	cggcagaacg	acctgtgtcc	ctggaagaga	gaaagaagca	gatagcgag	420
ctggcagaga	tggaattgc	tatcccggac	gaataccgtg	gtgaactcgc	gctcgctggc	480

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gaatggcaga cggatatccga acgagttatt cgaccagatg acgatacaga ggaaggaaaag 540
cctggtagct ctatcggcgt tcggaacgc aagatggaag gcgatgagga ggagcaggag 600
gcgcgacagg aggccgagag attcgtgagt caggggtggg gctcgaggac tcggcagtat 660
cctggggagc agagcgatgc agacctggat gcacttctaa attctaccaa ggatgtaaaag 720
aaggtcaagt tgcggcgcc ggatgaaggg tcgaaagaga aggctagcaa agagggtgct 780
acaccaagca acgatacggg ccaggctgcg gctcaggagt cagaactacc atcagtcaag 840
tctgagggtg aagaagcggc gcagcttgct acaacagata cccagcggg gaagcaggaa 900
gaggaggcgg cacctacagg agttgtttt aagaagcgca agccgaagg cctgaggaaa 960
tag

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<210> 181

<211> 876

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.2; clone 5-3-11; contig 4839 region 12269-14135
Coding region without introns

<400> 181

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cgggatacac ccttcgagaa aaccagcat gaagcgagt ccaaacacca gggaaacctt 120
aagcgtttcc tacgagatat ccaccgggaa aatgaacgga agcaaagaga aactcagaag 180
gcgaaggatg aagtcgagcg attaaggcaa actgtcgag gaaaaccagg tgcaaaagac 240
agcggcgcaa cagcttgaa acacgcctcg gctgcccctc caccggcaga acgacctgtg 300
tccctggaag agagaaagaa gcagatagcg cagctggcag agatgggaat tgctatccc 360
gacgaatacc gtggtgaact cgcgctcgt ggcgaatggc agacggtatc cgaacgagtt 420
attcgaccag atgacgatac agaggaaagg aagcctggta gctctatcgg cgttcggaaa 480
cgcaagatgg aaggcgatga ggaggagcag gaggcgcgac aggaggccga gagattcgtg 540
agtcagggtt gggctcgag gactcggcag taccctgggg agcagagcga tgcagacctg 600
gatgcacttc taaattctac caaggatgta aagaaggtca agttgtcggc gccggatgaa 660
gggtcgaaaag agaaggttag caaagagggt gctacaccaa gcaacgatac ggaccaggct 720
gcggctcagg agtcagaact accatcagtc aagtctgagg gtaaaagaagc ggcgagctt 780
gctacaacag ataccccgag ggtgaagcag gaagaggagg cggcacctac aggagttgtt 840
tttaagaagc gcaagccgaa ggtcctgagg aaatag 876

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<210> 182

<211> 291

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.2; clone 5-3-11; contig 4839 region 12269-14135
Protein sequence

<400> 182

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Met Ala Glu Tyr Trp Lys Ser Ala Pro Arg Phe Trp Cys Lys Gln Cys
1           5           10           15

Lys Ile Phe Ile Arg Asp Thr Pro Phe Glu Lys Thr Gln His Glu Ala
20           25           30

Ser Ala Lys His Gln Gly Asn Leu Lys Arg Phe Leu Arg Asp Ile His
35           40           45

Arg Glu Asn Glu Arg Lys Gln Arg Glu Thr Gln Lys Ala Lys Asp Glu
50           55           60

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Val Glu Arg Leu Arg Gln Thr Val Ala Gly Lys Pro Gly Ala Lys Asp
65 70 75 80

Ser Gly Ala Thr Ala Trp Lys His Ala Ser Ala Ala Pro Pro Pro Ala
85 90 95

Glu Arg Pro Val Ser Leu Glu Glu Arg Lys Lys Gln Ile Ala Gln Leu
100 105 110

Ala Glu Met Gly Ile Ala Ile Pro Asp Glu Tyr Arg Gly Glu Leu Ala
115 120 125

Leu Ala Gly Glu Trp Gln Thr Val Ser Glu Arg Val Ile Arg Pro Asp
130 135 140

Asp Asp Thr Glu Glu Gly Lys Pro Gly Ser Ser Ile Gly Val Arg Lys
145 150 155 160

Arg Lys Met Glu Gly Asp Glu Glu Glu Gln Glu Ala Arg Gln Glu Ala
165 170 175

Glu Arg Phe Val Ser Gln Gly Trp Gly Ser Arg Thr Arg Gln Tyr Pro
180 185 190

Gly Glu Gln Ser Asp Ala Asp Leu Asp Ala Leu Leu Asn Ser Thr Lys
195 200 205

Asp Val Lys Lys Val Lys Leu Ser Ala Pro Asp Glu Gly Ser Lys Glu
210 215 220

Lys Ala Ser Lys Glu Gly Ala Thr Pro Ser Asn Asp Thr Asp Gln Ala
225 230 235 240

Ala Ala Gln Glu Ser Glu Leu Pro Ser Val Lys Ser Glu Gly Lys Glu
245 250 255

Ala Ala Gln Leu Ala Thr Thr Asp Thr Pro Ala Val Lys Gln Glu Glu
260 265 270

Glu Ala Ala Pro Thr Gly Val Val Phe Lys Lys Arg Lys Pro Lys Val
275 280 285

Leu Arg Lys
290

<210> 183

<211> 2193

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.1; clone 10-4-20; contig 4929 region 328110-325663
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 183

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aacggaggct	gttaagttat	cgccacgggg	aaatagccca	aaaggaactc	gtcacagctg	120
gaatcaacac	caagtaccga	agaaacaagc	gagcagcggc	tgtttggtt	ctgcagctgc	180
acaaaaaatg	ggaacgaagt	gaatgaggtt	agatagagat	gaggatggat	caagaagcgc	240
cctccagatg	tagcaatgaa	gagatgatgt	tgcaagaaga	ggtgaaacaa	gctggcggca	300

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cgggatcagg ctaggctaga tagggtagc aacgagggtg acatcacgtg agaacgggca 360
tcgtgatatg gatgacaatt aacatcataa acactcttcg ttcagttgct gtgactcctg 420
acgcgtaagg ggatctgggg tgaagtcaag caatagactc tctgacagat ttgactttag 480
agaaagtaaa taacaccact atggacatct cgcaagaaac cgttgataaa atacgacgtt 540
tcgcgcaaaa gcgcaaaaaa gcggaggagt tctacgagga acactcggta aatccagcta 600
atthttgacgc ttacaatcgc aagttggatg agacgttggc agagctgcag gctcaagtca 660
aacgtcatga ggatgagctc cgcaaggtag gtcaacaagt tgcctagaat ataagccgac 720
tgtcacaaga gatttcatgc atgaattagg aatactgaca agaggacag ctacgcatga 780
ccaccacgat cgagttcgct caaattgggg cagatccttg ggcccgcac tcagaagtgc 840
gcagagccaa gaaagcgtat gattctcttc tgcaatcgga aacgcgactg ccgagtcag 900
gctcgccctt gccttcatta cttgcggttg acgaggcgtc tcgtctcgtc aaggagagca 960
agactcctaat ctactgacg gcggagaaac tgtctcgga tcgtcagcgc ttgaaagcgg 1020
aagaagccaa tttgcgcgat gcgcaactga tcaaagacgg gttggagaaa aggattgagc 1080
ggctgaacgc agaaaaatcg agtcaagtc agaaaaactc tgccgagctt gcgtatgatc 1140
tcgtcaagga gcagcaggaa aagatcgaga gacttgatac taccacagaa gagctaaagt 1200
cctctctcta taaatttgtc gaagacacac ttgcccacat gcttgctgca gaaaatctgg 1260
gcggtccac tgtcgagat gcgttggaat tttcgacac taccttaaaa gcgggctaca 1320
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aacagcggat tgacgagctt gttcgctgcc aaactgcgca ggaggcaac gagcaggcaa 1440
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tagatgcgga ttactcctat gtcgaccttc cgcagagtc agcggcctcg cgctttctag 1560
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caacgaagaa gcggccccga aagccactgg tagcataacg ccttgagaat gcgagagata 1860
catcaaaagc ttatcagaaa gttcaatgct cgaggtaaaa aatataccgt taatgccata 1920
caagaacat ggaagaagaa agaccgtagc cgggtatcag atcggcatca ttccgatgct 1980
ggtagaagta ctcttgccg tattctttgc tttggagcca gttcgggaac ccgccgagcg 2040
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ccctgtagcg ttcttgcggt ggaagcgctt cttggacgaa gtctttcttt tcttggaacg 2160
gctagtctcg gtgtcttcat actcttcgga tga 2193

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<210> 184

<211> 1448

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.1; clone 10-4-20; contig 4929 region 328110-325663
 Genomic sequence containing the coding region

<400> 184

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ggaaacgagt cggagaccta tacggatgcc aaggctgagc cttccgctgc gccaaagtgt 180
actgctgatg gccagggcga cactgttgtt cctgatgctc caaatggtaa ggggtgcatcc 240
acggagacgc agccaattca gtcgaccgog tctcatggcg agcgcgctac ttctcagccc 300
gaacagcagc gccacaaga tgaatccagc tggattcaca ttcgcgctgt aatttctagc 360
caggaagctg ccacagtcac tggcaagggt ggagaaaacg tatctcagat tcgtcgttt 420
tctggagcaa agtgacactgt cagcgactac tcccgtgggt cagtcgaacg tattttgacc 480
gtgagcggcc cacaggatgc cggtgccaa gttgggtttt tgatctatcc ttcgctgttt 540
gaaagattgc taattcagag taggcgtttg gtttgatcat ccgtacattg aacaatgaac 600
ctcttgatgc cccctctacc gcccaatcca agacataccc tctgcgtttg ctgatcccc 660
atctccttat tggctccatc attggcaaa gttggttcac cattcgcgaa attcaggaa 720
cttctggtgc ccgactgaat gcatccgatt cgtgccttcc cttgtcctct gagcggtcac 780
ttgtaattct cggcggttgc gattctgtcc acatcgctac ctactacgtc gccgtaacc 840
tcgttagcga gctcactgag cgctttggag gtctcgagc ctcagcttat gccactcgca 900
gcgggtggcc tgctggagca gtgcctggcg gtatgcaggt tgtcccgtat gttccacagc 960
ccgctggtgg tcaatatggc catccagaac atttcaagag acaccatcac caccccaatc 1020

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gcgctgctgc aggcgcctat ggggtccctt accttcacgg tcagcctgct cccgcaccag 1080
tgcccagcc ggctttgcat tatggagctg ctcccatgca cccttacgca ggagctggcc 1140
cccatcagcc tgctccatac ggcgcaccgc agcccgctca ggcacgcggc gctcctaccc 1200
ctgccacacc cgttgagggt gtcatgcctg gtcagccatt gactcagcag atctacatcc 1260
ccaacgacat ggttggtgcc atcatcggaa agggcggtgc gaagatcaat gagattcgac 1320
acctcagtgg cagtgtgatc aagattaatg agcctcaaga gaacagcaat gagcgtttgg 1380
tgactattac tggaaccag gaatgcaacc aaatggctct gtacatgctt tactcgcgac 1440
ttggttag

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<210> 185

<211> 1395

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.1; clone 10-4-20; contig 4929 region 328110-325663
Coding region without introns

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<400> 185
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ggaaaacgagt cggagacctt tacggatgcc aaggctgagc ctcccgctgc gccaagtgtc 180
actgctgatg gccagggcga cactgttgtt cctgatgctc caaatggtaa ggggtgcatcc 240
acggagacgc agccaattca gtcgaccgcg tctcatggcg agcgcgctac ttctcagccc 300
gaacagcagc gccacaaga tgaatccagc tggattcaca ttccgctgt aatttctagc 360
caggaagctg ccacagtcac tggcaagggt ggagaaaacg tatctcagat tcgtcgtttg 420
tctggagcaa agtgactgt cagcgactac tcccgtggtg cagtcgaacg tattttgacc 480
gtgagcggcc cacaggatgc cgttgccaag gcgtttggtt tgatcatccg tacattgaac 540
aatgaacctc ttgatgcccc ctctaccgcc caatccaaga cataccctct gcgtttgctg 600
atcccccatc tccttattgg ctccatcatt ggcaaagggt gttcacgcac tcgcgaaatt 660
caggaagctt ctggtgcccg actgaatgca tccgattcgt gccttcctt gtccctctgag 720
cggtcacttg taattctcgg cgttgccgat tctgtccaca tcgctacctt ctacgtcgcc 780
gtaacctcgc ttgacagct cactgagcgc tttggaggtc ctgcagcctc agcttatgcc 840
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ccacagcccg ctggtggtca atatggccat ccagaacatt tcaagagaca ccatcaccac 960
cccaatcgcg ctgctgcagg cgcctatggg gtcccttacc ttacaggtca gcctgctccc 1020
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gttggtcccc atcagcctgc tccatacggc gcaccgcagc ccgctcagga acgcggcgct 1140
cctaccctcg ccacaccgt tggaggtgtc atgctgggtc agccattgac tcagcagatc 1200
taccatccca acgacatggt tggtgccatc atcgaaaagg gcggtgcgaa gatcaatgag 1260
attcgacacc tcagtggcag tgtgatcaag attaatgagc ctcaagagaa cagcaatgag 1320
cgtttggtga ctattactgg aaccaggaat tgcaacccaa tggtctctga catgctttac 1380
tcgcgacttg gtttag

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<210> 186

<211> 464

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.1; clone 10-4-20; contig 4929 region 328110-325663
Protein sequence

<400> 186

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Met Ser Ala Ser Pro Ser Ala Leu Gln Ser Thr Lys Arg Pro Leu Glu
1           5           10           15

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Asp Pro Ser Ser Pro Ser Gly Pro Asn Asp Gln Pro Glu Ala Lys Arg

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20					25					30					
Pro	Ala	Leu	Asp	Lys	Val	Val	Lys	Gly	Asn	Glu	Ser	Glu	Thr	Tyr	Thr
35					40					45					
Asp	Ala	Lys	Ala	Glu	Pro	Ser	Ala	Ala	Pro	Ser	Ala	Thr	Ala	Asp	Gly
50					55					60					
Gln	Gly	Asp	Thr	Val	Val	Pro	Asp	Ala	Pro	Asn	Gly	Lys	Gly	Ala	Ser
65					70					75					
Thr	Glu	Thr	Gln	Pro	Ile	Gln	Ser	Thr	Ala	Ser	His	Gly	Glu	Arg	Ala
85					90					95					
Thr	Ser	Gln	Pro	Glu	Gln	Gln	Arg	Pro	Gln	Asp	Glu	Ser	Ser	Trp	Ile
100					105					110					
His	Ile	Arg	Ala	Val	Ile	Ser	Ser	Gln	Glu	Ala	Ala	Thr	Val	Ile	Gly
115					120					125					
Lys	Gly	Gly	Glu	Asn	Val	Ser	Gln	Ile	Arg	Arg	Leu	Ser	Gly	Ala	Lys
130					135					140					
Cys	Thr	Val	Ser	Asp	Tyr	Ser	Arg	Gly	Ala	Val	Glu	Arg	Ile	Leu	Thr
145					150					155					
Val	Ser	Gly	Pro	Gln	Asp	Ala	Val	Ala	Lys	Ala	Phe	Gly	Leu	Ile	Ile
165					170					175					
Arg	Thr	Leu	Asn	Asn	Glu	Pro	Leu	Asp	Ala	Pro	Ser	Thr	Ala	Gln	Ser
180					185					190					
Lys	Thr	Tyr	Pro	Leu	Arg	Leu	Leu	Ile	Pro	His	Leu	Leu	Ile	Gly	Ser
195					200					205					
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210					215					220					
Gly	Ala	Arg	Leu	Asn	Ala	Ser	Asp	Ser	Cys	Leu	Pro	Leu	Ser	Ser	Glu
225					230					235					
Arg	Ser	Leu	Val	Ile	Leu	Gly	Val	Ala	Asp	Ser	Val	His	Ile	Ala	Thr
245					250					255					
Tyr	Tyr	Val	Ala	Val	Thr	Leu	Val	Glu	Gln	Leu	Thr	Glu	Arg	Phe	Gly
260					265					270					
Gly	Pro	Ala	Ala	Ser	Ala	Tyr	Ala	Thr	Arg	Ser	Gly	Gly	Pro	Ala	Gly
275					280					285					
Ala	Val	Pro	Gly	Gly	Met	Gln	Val	Val	Pro	Tyr	Val	Pro	Gln	Pro	Ala
290					295					300					
Gly	Gly	Gln	Tyr	Gly	His	Pro	Glu	His	Phe	Lys	Arg	His	His	His	His
305					310					315					
Pro	Asn	Arg	Ala	Ala	Ala	Gly	Ala	Tyr	Gly	Val	Pro	Tyr	Leu	His	Gly
325					330					335					
Gln	Pro	Ala	Pro	Ala	Pro	Val	Ala	Gln	Pro	Ala	Leu	His	Tyr	Gly	Ala
340					345					350					

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Ala Pro His Ala Pro Tyr Ala Gly Ala Gly Pro His Gln Pro Ala Pro
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Tyr Gly Ala Pro Gln Pro Ala Gln Ala Arg Gly Ala Pro Thr Pro Ala
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Thr Pro Val Gly Gly Val Met Pro Gly Gln Pro Leu Thr Gln Gln Ile
 385 390 395 400

Tyr Ile Pro Asn Asp Met Val Gly Ala Ile Ile Gly Lys Gly Gly Ala
 405 410 415

Lys Ile Asn Glu Ile Arg His Leu Ser Gly Ser Val Ile Lys Ile Asn
 420 425 430

Glu Pro Gln Glu Asn Ser Asn Glu Arg Leu Val Thr Ile Thr Gly Thr
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Gln Glu Cys Asn Gln Met Ala Leu Tyr Met Leu Tyr Ser Arg Leu Gly
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<210> 187

<211> 2121

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.2; clone 10-4-20; contig 4839 region 328075-330267
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 187

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tgacaattaa	catcataaac	actcttcggt	cagttgctgt	gactcctgac	gcgtaagggg	360
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acaccactat	ggacatctcg	caagaaaccg	ttgataaaat	acgacgtttc	gcgcaaaagc	480
gccccaaaagc	ggaggagtgc	tacgaggaac	actcggtaaa	tccagctaata	tttgacgctt	540
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atgagctccg	caaggtagct	caacaagttg	cctagaatat	aagccgactg	tcacaagaga	660
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atctcaccaa	acatctggga	aaagacaaac	agacgccatc	cccacggata	tatagcgact	1680
caaccgaaag	ccagtaagat	atctagagcc	ggcgaaaacc	acgtgtttca	acgaagaagc	1740

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aagaagaaag accgtagccg ggtatcagat cggcatcatt ccgatgctgg tagaagtact 1920
cttggccgta ttctttgctt tggagccagt tcgggaaccc gccgagcgct tgttgacttg 1980
atcgttggc tcccttctag gtcgcgccgt ttttattttt gaactcgacc ctgtagcgtt 2040
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gtcttcatac tcttcggatg a 2121

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<210> 188

<211> 1143

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.2; clone 10-4-20; contig 4839 region 328075-330267
Genomic sequence containing the coding region

<400> 188

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aagttggatg agacgttggc agagctgcag gctcaagtca aacgtcatga ggatgagctc 180
cgcaaggtac gtcaacaagt tgcttagaat ataagccgac tgtcacaaga gatttcatgc 240
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caaattgggg cagatccttg ggcccgcac tcagaagtgc gcagagccaa gaaagcgtat 360
gattctcttc tgcaatcgga aacgcgactg ccgagtcacg gctcgccctt gccttcatta 420
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gcgcaactga tcaaagacgg gttggagaaa aggattgagc ggctgaacgc agaaaaatcg 600
agtcaagtcc agaaaactcc tgcgcagctt gcgtatgatc tcgtcaagga gcagcaggaa 660
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gcgttggaat tttcggacac taccttaaaa gcgggctaca ctagccatgg gaagcctaag 840
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gtcgaccttc cgcacgagtc agcggcctcg cgctttctag taagagcgaa ggtagctcaa 1080
ttccatccgc gcgatgccag gaagcttcgg ttaattgatt ttgggcgctc attagtcgat 1140
tga 1143

```

<210> 189

<211> 1035

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.2; clone 10-4-20; contig 4839 region 328075-330267
Coding region without introns

<400> 189

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aagttggatg agacgttggc agagctgcag gctcaagtca aacgtcatga ggatgagctc 180
cgcaaggtac gtcaacaagt tgcttagaat ataagccgac tgtcacaaga gatttcatgc 240
aagaaagcgt atgattctct tctgcaatcg gaaacgcgac tgccgagtc aggctcgccc 300
ttgccttcac tacttgcggt tgacgaggcg tctcgtctcg tcaaggagag caagacctca 360
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aatgtgcgag atgcgcaact gatcaaagac gggttgagga aaaggattga gcggctgaac 480
gcagaaaaat cgagtcaagt ccagaaaact cctgcgcagc ttgcgtatga tctcgtcaag 540
gagcagcagg aaaagatcga gagacttgat actaccacag aagagctaaa gtcctctctc 600

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tataaatttg tcgaagacac acttgcccca atgcttgctg cagaaaatct gggcgggtccc 660
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gggaagccta agaaacccaaa aactccggcc gtggggactt ctgacagtgg ccaacagcgg 780
attgacgagc ttgttcgtcg ccaaactgcg caggagggca acgagcaggc aacccttttg 840
aacaaaagag aggcggccgc cgctgaaatg cgagctcttc ttactgctct gttagatgcg 900
gattactcct atgtcgacct tccgcacgag tcagcggcct cgcgctttct agtaagagcg 960
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tcattagtcg attga 1035

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<210> 190

<211> 344

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.2; clone 10-4-20; contig 4839 region 328075-330267
Protein sequence

<400> 190

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Ala Asn Phe Asp Ala Tyr Asn Arg Lys Leu Asp Glu Thr Leu Ala Glu
35        40        45

Leu Gln Ala Gln Val Lys Arg His Glu Asp Glu Leu Arg Lys Phe Ala
50        55        60

Gln Ile Gly Ala Asp Pro Trp Ala Arg Ile Ser Glu Val Arg Arg Ala
65        70        75        80

Lys Lys Ala Tyr Asp Ser Leu Leu Gln Ser Glu Thr Arg Leu Pro Ser
85        90        95

Pro Gly Ser Pro Leu Pro Ser Leu Leu Ala Val Asp Glu Ala Ser Arg
100       105       110

Leu Val Lys Glu Ser Lys Thr Ser Ile Ser Leu Thr Ala Glu Lys Leu
115      120      125

Ser Ala Asp Arg Gln Arg Leu Lys Ala Glu Glu Ala Asn Leu Arg Asp
130      135      140

Ala Gln Leu Ile Lys Asp Gly Leu Glu Lys Arg Ile Glu Arg Leu Asn
145      150      155      160

Ala Glu Lys Ser Ser Gln Val Gln Lys Thr Pro Ala Gln Leu Ala Tyr
165      170      175

Asp Leu Val Lys Glu Gln Gln Glu Lys Ile Glu Arg Leu Asp Thr Thr
180      185      190

Thr Glu Glu Leu Lys Ser Ser Leu Tyr Lys Phe Val Glu Asp Thr Leu
195      200      205

Ala Pro Met Leu Ala Ala Glu Asn Leu Gly Gly Pro Thr Val Gly Asp
210      215      220

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Ala Leu Glu Ile Ser Asp Thr Thr Leu Lys Ala Gly Tyr Thr Ser His
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 245 250 255

Gly Gln Gln Arg Ile Asp Glu Leu Val Arg Arg Gln Thr Ala Gln Glu
 260 265 270

Gly Asn Glu Gln Ala Thr Leu Leu Asn Lys Arg Glu Ala Ala Ala Ala
 275 280 285

Glu Met Arg Ala Leu Leu Thr Ala Leu Leu Asp Ala Asp Tyr Ser Tyr
 290 295 300

Val Asp Leu Pro His Glu Ser Ala Ala Ser Arg Phe Leu Val Arg Ala
 305 310 315 320

Lys Val Ala Gln Phe His Pro Arg Asp Ala Arg Lys Leu Arg Leu Ile
 325 330 335

Asp Phe Gly Arg Ser Leu Val Asp
 340

<210> 191
 <211> 2000
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA283; clone 11-6-20; contig 4910 region 9638-11637
 Genomic sequence containing 3' and 5'-ends and the coding region

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 ctttcgattg tgaatccact tctccatttt taactccatt taatcaatac 1440
 ctctcgatg gggtaaatca atgcaccgga aatttacata tgatatcaaa agtagtagtt 1500
 ctccgactag ggaggatgga gcaaggtaat ctatatattt tggctgctcg tttgcaggcc 1560

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PCT/IB03/01374

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<210> 192

<211> 4336

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> ATPase; Phylum CEA284.1; clone 4-3-4; contig 4899

region 472441-476776

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 192

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PCT/IB03/01374

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<212> DNA

<213> *Aspergillus fumigatus*

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<223> ATPase; Phylum CEA284.1; clone 4-3-4; contig 4899

region 472441-476776

Genomic sequence containing the coding region

<400> 193

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<212> DNA

<213> *Aspergillus fumigatus*

<220>

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region 472441-476776

Coding region without introns

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<210> 195

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<213> *Aspergillus fumigatus*

<220>

<223> ATPase; Phylum CEA284.1; clone 4-3-4; contig 4899

region 472441-476776

Protein sequence

<400> 195

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PCT/IB03/01374

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PCT/IB03/01374

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PCT/IB03/01374

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<210> 196

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<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Homologue GmZnfl; Phylum CEA284.2;

contig 4899 region 477626-479684

Genomic sequence containing 3' and 5'-ends and the coding region

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contig 4899 region 477626-479684
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contig 4899 region 477626-479684
Coding region without introns

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 contig 4899 region 477626-479684
 Protein sequence

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          35          40          45

Cys Glu Val Thr Cys Tyr Gly Tyr Ala Pro Ser Gln Arg Arg Arg Cys
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Arg Met Arg Thr Arg Lys Asp Asn Arg Asp Arg Ala Ser Tyr Leu Leu
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Glu Glu Gly Thr Arg Tyr Leu Gln Arg Gly Leu Pro Val Asp Gly Leu
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Leu Ile Glu Leu Ala Pro Leu Val Leu Cys Thr Arg Phe His Gln Tyr
          100          105          110

Gln Ala Asp Asp Leu Val Arg Asp Trp Arg Ala Lys Leu Arg Glu Phe
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Gln Gln Gln Thr Leu Leu Asn Ala Met Leu Lys Ser Leu Gln Glu Leu
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Val Asp Ser Arg Ala Arg Ser Arg Ala Ala Arg Ser Ala Gly Arg Arg
145          150          155          160

Leu Pro Glu Arg Val Ser Ser Pro Thr Arg Leu Glu Arg Ser Ala Ala
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Ile Val Thr Glu Glu Glu Pro Ala Ala Pro Glu Arg Glu Glu Glu Glu
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Glu Glu Arg Gly Asp Arg Glu Asp Glu Pro Glu Pro Glu Pro Glu Pro
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Glu Pro Glu Leu Thr Pro Ser Arg Ser Ser Thr Glu Thr Ser Ser Pro
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Ala Val Glu Ala His Val Ala Glu Pro Thr Val Pro Gln Thr Glu Ser
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275 280 285

Thr Ala Ser Asp Glu His Asp Ala Pro Glu Glu His Asp Asp Asp Asp
290 295 300

Leu Val Tyr Cys Lys Asn Gln Cys Gly Thr Asn Tyr His Lys Ala Cys
305 310 315 320

Ile Asp Val Trp His Ala Thr Gln Arg Thr Phe Glu Thr Pro Arg Gly
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